

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 10:17:03 ; Search time 24.6053 Seconds
(without alignments)
1075.364 Million cell updates/sec

Title: US-08-949-904A-3
Perfect score: 1487
Sequence: 1 SARGGLFLGQDFSYKRSNC.....WQKGQREFKRISIRKLQC 275
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1487	100.0	295	2 JE0174	frizzled protein-2
2	614	41.3	317	2 JE0175	frizzled protein-1
3	270.5	18.2	568	2 T25162	Frizzled-1 protein
4	269	18.1	647	2 JE0337	Frizzled-1 protein
5	264.5	17.8	537	2 JC7127	Frizzled protein 4
6	264.5	17.8	574	2 JE0339	Frizzled-7 protein
7	264.5	17.8	581	2 JC7086	PZD10 protein - hu
8	263.5	17.7	550	2 T37325	wingless protein r
9	259.5	17.5	641	2 A45054	probable intercell
10	256.5	17.2	565	2 JE0338	Frizzled-2 protein
11	241	16.2	694	2 S71786	wingless receptor
12	224.5	15.1	605	2 T31690	hypothetical prote
13	222	14.9	581	2 S03540	gene frizzled prot
14	216.5	14.6	666	2 JC7312	frizzled-3 protein
15	216.5	14.6	1113	2 JE0315	low-density lipopr
16	205.5	13.8	197	2 JC7735	frizzled-related p
17	201	13.5	706	2 JE0164	frizzled-6 protein
18	177.5	11.9	579	2 JC7629	membrane-type friz
19	149.5	10.1	1774	2 B56101	collagen alpha 1(X
20	133.5	9.0	526	2 T13484	frizzled protein h
21	119	8.0	581	2 B54665	netrin-2 precursor
22	96.5	6.5	793	2 JC5539	Smoothed protein
23	95.5	6.4	1282	2 JE0120	Glycoprotein A - m
24	91	6.1	532	2 AE1964	Dnak-type molecula
25	91	6.1	1290	2 A55094	chromosomal protei
26	89.5	6.0	392	2 E81325	probable dihydroor
27	88.5	6.0	301	2 AC1989	hypothetical prote
28	88.5	6.0	606	2 A54665	netrin-1 precursor
29	88	5.9	3724	2 T18427	hypothetical prote

30	87.5	5.9	338	2 D97166	flagellar motor sw
31	87.5	5.9	366	2 D45558	epidermal growth f
32	87	5.9	761	2 D70447	tetrahydropteroylt
33	87	5.9	1014	2 T30545	major surface glyco
34	86.5	5.8	371	2 T34410	hypothetical prote
35	86.5	5.8	640	2 T19346	hypothetical prote
36	86.5	5.8	1342	2 A36223	kinase-related tra
37	86.5	5.8	2643	2 T29149	hypothetical prote
38	86	5.8	413	2 S52610	TYA protein - yeast
39	86	5.8	800	2 S13032	3',5'-cyclic-GMP p
40	86	5.8	856	2 S30762	3',5'-cyclic-GMP p
41	85.5	5.7	661	2 T42754	hypothetical prote
42	85	5.7	240	2 T33698	hypothetical prote
43	84.5	5.7	425	2 I59355	synaptotagmin IV -
44	84.5	5.7	727	2 T23585	hypothetical prote
45	84.5	5.7	1024	2 S71804	receptor-like serp

ALIGNMENTS

RESULT 1

JE0174
frizzled protein-2 - human
C:Species: Homo sapiens (man)
C>Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C:Accession: JE0174
R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.
Biochem. Biophys. Res. Commun. 247, 287-293, 1998
A>Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.
A:Reference number: JE0174; MUID:98308108; PMID:9642118
A:Accession: JE0174
A:Molecule type: mRNA
A:Residues: 1-295 <HUA>
A:Cross-references: UNIPROT:Q9HAP5
C:Genetics:
A:Map position: 4q

Query Match	100.0%	Score 1487;	DB 2;	Length 295;
Best Local Similarity	100.0%	Pred. No. 1.5e-110;		
Matches 275;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	SARGGLFLGQDFSYKRSNC	KPIPANLQCHGIEYQNNRMLPNLLGHETMKEVLEQAGAWI	60
Db	21	SARGGLFLGQDFSYKRSNC	KPIPANLQCHGIEYQNNRMLPNLLGHETMKEVLEQAGAWI	80
QY	61	PLVMKQCHPDTKFLCSL	FAVCLDDDETTPCHSLCVQVKDRCAPVMSAFGPPWDM	120
Db	81	PLVMKQCHPDTKFLCSL	FAVCLDDDETTPCHSLCVQVKDRCAPVMSAFGPPWDM	140
QY	121	ECDRFPQNDLCIPLASSD	HLLPATEAPKVCACKNNDDNDIMETLCKNDFAKTKV	180
Db	141	ECDRFPQNDLCIPLASSD	HLLPATEAPKVCACKNNDDNDIMETLCKNDFAKTKV	200
QY	181	KEITYINRDTKIILETSK	TIYKLVNGVSRDLKKSVMWLKDSLOCTCEMNDINAPYLV	240
Db	201	KEITYINRDTKIILETSK	TIYKLVNGVSRDLKKSVMWLKDSLOCTCEMNDINAPYLV	260
QY	241	QKGQGGELVITSVRKWK	QGQREFKRISIRKLQC	275
Db	261	QKGQGGELVITSVRKWK	QGQREFKRISIRKLQC	295

RESULT 2

JE0175
frizzled protein-1b - human
C:Species: Homo sapiens (man)
C>Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C:Accession: JE0175
R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.
Biochem. Biophys. Res. Commun. 247, 287-293, 1998
A>Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.
A:Reference number: JE0174; MUID:98308108; PMID:9642118

RESULT 8
T37325
wingless protein receptor Cfz2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T37325
R/Sato, A.; Kojima, T.; Ui-Tei, K.; Miyata, Y.; Saigo, K.
Development 126, 4421-4430, 1999
A/Rittle: Dfrizzled-3, a new Drosophila Wnt receptor, acting as an attenuator of
A/Reference number: Z21689; PMID:99429803; PMID:10498678
A/Accession: T37325
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-550 <SAT>
A/Cross-references: UNIPROT:Q9UBU6; EMBL:AB026113; NID:G5931529; PIDN:BAA84678
C/Genetics:
A/Gene: Cfz2

C;Superfamily: fruit fly trilled protein
C;Keywords: receptor; signal transduction; transmembrane protein

Query Match 17.7%; Score 263.5; DB 2; Length 550;
Best Local Similarity 33.8%; Pred.No. 3.le-13;

Matches 54; Conservative 29; Mismatches 62; Indels 15; Gaps 4;

QY 7 LFGQPDFSYSKRSCKIPANLQLCHGIEYQNMBLPNLLGHETWKVEUQAAGATPLVMVKQ 66
||| ||| ||| : |
Db 18 LFG-----KRKCEGI--TIPLCKIGIVNTSPFNSYGHEKEOBEAEGLEVHQFYFLPEVG 69
||| ||| ||| : |

QY 67 CHPDTKKFELCSLFAPVLCDLDLETIOPHLSLCVQVDRCAPVMSAFGPWPMLECCRFP 126
||| ||| ||| : |
Db 70 CQGLHAAFFLTCTWTPTICQENYDRPIILPCMELCWARSKSFSIMAKYGRWPETUSCALP 129
||| ||| ||| : |

QY 127 QNDNLICIPASSDHLPLATEEAPKVCEA----CRKNKDNN 163
::: :::
Db 130 KMSD-----QMSTGNICAAPPDTFKQHKGHHHKNONON 165
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130 KMSD-----QMSUIGNICAAFPDPKQKHGHHHKNQNNQN 165

RESULT 9
A45054
probable intercellular signal transducer or transmitter Pz-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 02-Mar-2001
C:Accession: A45054
R;/Chan, S.D.; Karpf, D.B.; Fowlkes, M.E.; Hooks, M.; Bradley, M.S.; Vuong, V.;
J. Biol. Chem. 267, 25202-25207, 1992
A:Title: Two homologs of the Drosophila polarity gene frizzled (fz) are widely
A:Reference number: A45054, MUID:93094228; PMID:1334084
A:Accession: A45054
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-641 <CHA>
A:Experimental source: UMR 106 osteosarcoma cell line
A:Note: sequence extracted from NCBI backbone (NCBIP:120154)
C:Superfamily: fruit fly frizzled protein

Query Match 17.5%; Score 259.5; DB 2; Length 641;
Best Local Similarity 37.3%; Pred. No. 7.7e-13;

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Matches 56; Conservative 27; Mismatches 54; Indels 13; Gaps 6;
Qy 3 RGLFLFGQDDSYKRSNCKPPIANLQICHGIEYQNMRLPNLLGHETMKEVLEQAGAWIPL 62
Db 101 RGISI---PDHG-----CQPI--SIPLCIDIAYNOTIMPNLLGHTNQDAGLEVHQFYPL 151
Qy 63 VMKQCHPDTKFLCSLFAVCLDDDETIOQCHSLCVQVKRCAPVMSAFGFPWPDMLC 122
Db 152 VKVQCSAELKFLCSMYAPVC-TVLEQALPPCRSLCERAQG-CEALMKNKFGQWPDILKC 209
Qy 123 DRFPQD--NDLCIPLASSDHLPLPATEAPK 150
Db 210 EKFPVHGRGELCVGQNTSDKGTPTPSLLPE 239
RESULT 10
JE0338
Frizzled-2 protein - human
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1993 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C:Accession: JE0338
R:Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A:Title: Molecular cloning, differential expression, and chromosomal localization of human frizzled-2
A:Reference number: JE0337; MUID:99032814; PMID:9813155
A:Accession: JE0338
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-565 <SAG>
A:Cross-references: UNIPROT:Q14332; DDBJ:AB017364; NID:g3927884; PIDN:BAA34667.1; PID:g3927884
C:Superfamily: fruit fly frizzled protein
Query Match 17.2%; Score 256.5; DB 2; Length 565;
Best Local Similarity 36.8%; Pred. No. 1.1e-12;
Matches 50; Conservative 26; Mismatches 51; Indels 9; Gaps 4;
Qy 11 PDFSYKRSNCKPPIANLQICHGIEYQNMRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPD 70
Db 34 PDHGF----CQPI--SIPLCIDIAYNOTIMPNLLGHTNQDAGLEVHQFYPLVKVQCSPE 87
Qy 71 TKKFLCSLFAVCLDDDETIOQCHSLCVQVKRCAPVMSAFGFPWPDMLC DRFPQD-- 128
Db 88 LRFFLCSMYAPVC-TVLEQALPPCRSLCERAQGCEALMKNKFGQWPERLCRHEHFRHGA 146
Qy 129 NDLCIPLASSDHLPLA 144
Db 147 EQICVGNHSDGAPA 162
RESULT 11
S71786
wingless receptor precursor dfz2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: S71786; S78444
R:Bhanot, P.; Brink, M.; Harryman Samos, C.; Hsieh, J.C.; Wang, Y.; Macke, J.P.; Andrew,
Nature 382, 225-230, 1996
A:Title: A new member of the frizzled family from Drosophila functions as a wingless receptor
A:Reference number: S71786; MUID:96353971; PMID:8717036
A:Accession: S71786
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-694 <BHA>
A:Cross-references: UNIPROT:Q9VWX3; EMBL:U65589
A:Note: mRNA was also sequenced
R:Bhanot, P.; Wang, Y.; Nathans, J.
submitted to the EMBL Data Library, July 1996
A:Reference number: S78444
A:Accession: S78444
A:Molecule type: DNA
A:Residues: 1-416, 'T', 418-694 <BHW>
A:Cross-references: EMBL:U65589; NID:g1518050; PIDN:AAC47273.1; PID:g1518051
C:Genetics:

A:Gene: dfz2
A:Cross-references: FlyBase:FBgn0016797
C:Superfamily: fruit fly frizzled protein
C:Keywords: transmembrane protein
Query Match 16.2%; Score 241; DB 2; Length 694;
Best Local Similarity 35.3%; Pred. No. 2.5e-11;
Matches 49; Conservative 20; Mismatches 50; Indels 20; Gaps 5;
Qy 20 CKPIPANLQICHGIEYQNMRLPNLLGHETMKEV-LEQAGAWIPLVMKQCHPDTKFLCSL 78
Db 64 CEET--TIPMCRGIGYNTMTPNEMNHETQDEAGLEVHQFW-PLVEIKCSFDLKFPLCSM 120
Qy 79 FAPVCLDDDETIOQCHSLCVQVKRCAPVMSAFGFPWPDMLC DRFPQDND---LCIPL 135
Db 121 YTPCLEDYHKPLPVCRSVCERARSGCAPIMQISFEWPERMACEHLPLHGDPDNLCM-- 178
Qy 136 ASSDHLPLPATEAPKVCEA 154
Db 179 -----EQPSYTEA 186
RESULT 12
T31690
hypothetical protein F27E11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Mar-2001
C:Accession: T31690
R:Wansley, P.; Keppler, D.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid F27E11.
A:Reference number: Z21069
A:Accession: T31690
A:Status: preliminary; translated from GR/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-605 <WAM>
A:Cross-references: EMBL:AF016413; PIDN:AAB65257.1; GSPDB:GN00023; CESP:F27E11.3
A:Experimental source: strain Bristol N2; clone F27E11
C:Genetics:
A:Gene: CESP:F27E11.3
A:Map position: 5
A:Introns: 28/3; 454/1; 520/1; 562/1
C:Superfamily: fruit fly frizzled protein
Query Match 15.1%; Score 224.5; DB 2; Length 605;
Best Local Similarity 33.3%; Pred. No. 4.3e-10;
Matches 42; Conservative 27; Mismatches 50; Indels 7; Gaps 2;
Qy 41 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKFLCSLFAVCLDDDETIOQCHSLCVQ 100
Db 5 PMSYGHKQBEAGLEVHQFYPLVEVGCFOHLKFFLCTMYTPICQENYDKPLPCWELC 64
Qy 101 VKDRCAPVMSAFGFPWPDMLC DRFPQDNDLCIPLASSDHLPLPATEAPKVCEA---CKN 157
Db 65 ARSKCSPIKAKYGRWPDETLSCAELPKMSD---QMSTGNICAAAPDPTPKQKHGHHKN 120
Qy 158 KNDDDN 163
Db 121 QNQON 126
RESULT 13
S03540
Gene frizzled protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: S03540; S15708; S15709
R:Vinson, C.R.; Conover, S.; Adler, P.N.
Nature 338, 263-264, 1989
A:Title: A Drosophila tissue polarity locus encodes a protein containing seven potential transmembrane domains
A:Reference number: S03540; MUID:89159415; PMID:2493583
A:Accession: S03540
A:Status: not compared with conceptual translation

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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-949-904-3

Query Match 100.0%; Score 1487; DB 8; Length 275;
Best Local Similarity 100.0%; Pred. No. 9.5e-130;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRLPNLLGHETMKEVLEQAGAWI 60
DB 1 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRLPNLLGHETMKEVLEQAGAWI 60

QY 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKDRCAPVMSAFGFPWPDML 120
DB 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKDRCAPVMSAFGFPWPDML 120

QY 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDIMETLCKNDPALKIKV 180
DB 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDIMETLCKNDPALKIKV 180

QY 181 KEITYINRDTKIILETSKTIYKLVNGVSRDLKKSVMWLKDSLOCTCEEMNDINAPYLV 240
DB 181 KEITYINRDTKIILETSKTIYKLVNGVSRDLKKSVMWLKDSLOCTCEEMNDINAPYLV 240

QY 241 GOKGGELVITSVKRWKGQREFKRIIRSIRKLOC 275
DB 241 GOKGGELVITSVKRWKGQREFKRIIRSIRKLOC 275

RESULT 2
US-08-949-904-2
Sequence 2, Application US/08949904
Publication No. US20030175855A1
GENERAL INFORMATION:
APPLICANT: Lavallie, Edward
APPLICANT: Racie, Lisa
TITLE OF INVENTION: HUMAN SDF-5 PROTEIN AND COMPOSITIONS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS INSTITUTE, INC.
STREET: 87 CAMBRIDGE PARK DRIVE
CITY: CAMBRIDGE
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,904
FILING DATE: October 15, 1997
CLASSIFICATION: 336
ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, STEVEN R.
REGISTRATION NUMBER: 32,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-949-904-2

Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRLPNLLGHETMKEVLEQAGAWI 60
DB 21 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRLPNLLGHETMKEVLEQAGAWI 80

QY 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKDRCAPVMSAFGFPWPDML 120
DB 81 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKDRCAPVMSAFGFPWPDML 140

QY 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDIMETLCKNDPALKIKV 180
DB 141 ECDRFPQNDLCIPLASSDHLPPATEAPKVCCEACKNKNDNDIMETLCKNDPALKIKV 200

QY 181 KEITYINRDTKIILETSKTIYKLVNGVSRDLKKSVMWLKDSLOCTCEEMNDINAPYLV 240
DB 201 KEITYINRDTKIILETSKTIYKLVNGVSRDLKKSVMWLKDSLOCTCEEMNDINAPYLV 260

QY 241 GOKGGELVITSVKRWKGQREFKRIIRSIRKLOC 275
DB 261 GOKGGELVITSVKRWKGQREFKRIIRSIRKLOC 295

RESULT 3
US-10-177-293-142
Sequence 142, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavaru, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Pusztai, Lajos
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 142
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-293-142

Query Match 100.0%; Score 1487; DB 14; Length 295;
Best Local Similarity 100.0%; Pred. No. 1e-129;

Publication No. US20050049195A1
GENERAL INFORMATION:
APPLICANT: ZOU, YIMIN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION
FILE REFERENCE: ARCD:395US
CURRENT APPLICATION NUMBER: US/10/847,972
CURRENT FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/470,913
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 78
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens
US-10-847-972-78

Query Match 100.0%; Score 1487; DB 17; Length 295;
Best Local Similarity 100.0%; Pred. No. 1e-129;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGFLFGQPDFSYKRSNCKPDPANLQCHGIEYQNNRMLPNLLGHETWKEVLEQAGAWI 60
|||||
DB 21 SARGFLFGQPDFSYKRSNCKPDPANLQCHGIEYQNNRMLPNLLGHETWKEVLEQAGAWI 80
|||||

QY 61 PLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCQVKDRCAPVMSAFGFPWPDML 120
|||||
DB 81 PLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCQVKDRCAPVMSAFGFPWPDML 140
|||||

QY 121 ECDRFPQNDLCIPLASSDHLLPATEAPKVCCEACKNKNDNDIMETLCKNDFALKIKV 180
|||||
DB 141 ECDRFPQNDLCIPLASSDHLLPATEAPKVCCEACKNKNDNDIMETLCKNDFALKIKV 200
|||||

QY 181 KEITYINRDTKILLETSKTIYKLVNGVSRDLKKSVLMLKDSLOQTCCEMNDINAPYLVM 240
|||||
DB 201 KEITYINRDTKILLETSKTIYKLVNGVSRDLKKSVLMLKDSLOQTCCEMNDINAPYLVM 260
|||||

QY 241 GOKGGELVITSVKRWQKGOREFKRISIRKLOC 275
|||||
DB 261 GOKGGELVITSVKRWQKGOREFKRISIRKLOC 295
|||||

RESULT 7
US-10-432-256-2
Sequence 2, Application US/10432256
Publication No. US20050113291A1
GENERAL INFORMATION:
APPLICANT: Applied Research Systems ARS Holding N.V.
TITLE OF INVENTION: Use of SARP-1 in the treatment and/or prevention of scleroderma
FILE REFERENCE: EP 469 Y
CURRENT APPLICATION NUMBER: US/10/432,256
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens
US-10-432-256-2

Query Match 100.0%; Score 1487; DB 17; Length 295;
Best Local Similarity 100.0%; Pred. No. 1e-129;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGFLFGQPDFSYKRSNCKPDPANLQCHGIEYQNNRMLPNLLGHETWKEVLEQAGAWI 60
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DB 21 SARGFLFGQPDFSYKRSNCKPDPANLQCHGIEYQNNRMLPNLLGHETWKEVLEQAGAWI 80
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QY 61 PLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCQVKDRCAPVMSAFGFPWPDML 120
|||||
DB 81 PLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCQVKDRCAPVMSAFGFPWPDML 140
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QY 121 ECDRFPQNDLCIPLASSDHLLPATEAPKVCCEACKNKNDNDIMETLCKNDFALKIKV 180
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DB 141 ECDRFPQNDLCIPLASSDHLLPATEAPKVCCEACKNKNDNDIMETLCKNDFALKIKV 200
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QY 181 KEITYINRDTKILLETSKTIYKLVNGVSRDLKKSVLMLKDSLOQTCCEMNDINAPYLVM 240
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DB 201 KEITYINRDTKILLETSKTIYKLVNGVSRDLKKSVLMLKDSLOQTCCEMNDINAPYLVM 260
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QY 241 GOKGGELVITSVKRWQKGOREFKRISIRKLOC 275
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DB 261 GOKGGELVITSVKRWQKGOREFKRISIRKLOC 295
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RESULT 8
US-09-978-295A-415
Sequence 415, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.7%; Score 1483; DB 9; Length 295;
 Best Local Similarity 99.6%; Pred. No. 2.4e-129;
 Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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6	6	PRIOR FILING DATE: 1998-03-10	6	PRIOR APPLICATION NUMBER: 60/081838
7	7	PRIOR APPLICATION NUMBER: 60/077632	7	PRIOR FILING DATE: 1998-04-15
8	8	PRIOR FILING DATE: 1998-03-11	8	PRIOR APPLICATION NUMBER: 60/082568
9	9	PRIOR APPLICATION NUMBER: 60/077641	9	PRIOR FILING DATE: 1998-04-21
10	10	PRIOR FILING DATE: 1998-03-11	10	PRIOR APPLICATION NUMBER: 60/082569
11	11	PRIOR APPLICATION NUMBER: 60/077649	11	PRIOR FILING DATE: 1998-04-21
12	12	PRIOR FILING DATE: 1998-03-11	12	PRIOR APPLICATION NUMBER: 60/082704
13	13	PRIOR APPLICATION NUMBER: 60/077791	13	PRIOR FILING DATE: 1998-04-22
14	14	PRIOR FILING DATE: 1998-03-12	14	PRIOR APPLICATION NUMBER: 60/082804
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25	25	PRIOR APPLICATION NUMBER: 60/079294	25	PRIOR FILING DATE: 1998-04-28
26	26	PRIOR FILING DATE: 1998-03-25	26	PRIOR APPLICATION NUMBER: 60/083392
27	27	PRIOR APPLICATION NUMBER: 60/079656	27	PRIOR FILING DATE: 1998-04-29
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Query Match          99.7%; Score 1483; DB 9; Length 295;
Best Local Similarity 99.6%; Pred. No. 2.4e-129;
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SARGLFLFQOPDFSYKRSNCKIPANLQLCHGIEYQNMRLPNLLGHETTKVLEQAGAWI 60
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Db 21 SARGLFLFQOPDFSYKRSNCKIPVNLQLCHGIEYQNMRLPNLLGHETTKVLEQAGAWI 80
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QY 61 PLVMKQCHPDTTKFLCSLPAPVCLDDDETIOCHSLCVQVKDRCAPVMSAFGFPWDM 120
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QY 121 ECDRFPQNDLCTPLASSDHLHPATBEPKVCCEAKGNKNDNDIMETLCKNDFALKIKV 180
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QY 181 KEITYINRDTKIILETKSTIYKLVNGVSRRDLKKSVLWLKDSLQTCCEMNDINAPYLV 240
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QY 241 GQGGELVITSVKRWQKQREFKRSIRKLQC 275
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Db 261 GQGGELVITSVKRWQKQREFKRSIRKLQC 295
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RESULT 11
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; Publication No. US20020192706A1
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643

; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
; PRIOR APPLICATION NUMBER: 60/085697
Query Match 99.7%; Score 1483; DB 9; Length 295;
Best Local Similarity 99.6%; Pred. No. 2.4e-129;
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 SARGLFLFGQPDFSYKRSNCKPIPANLQLCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60
Db 21 SARGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80
Qy 61 PLVMKQCHPDTKFLCSLFPAPVCLDDLDDETIQPCHSILCVQVKDRCAPVNSAFGFPWPDML 120
Db 81 PLVMKQCHPDTKFLCSLFPAPVCLDDLDDETIQPCHSILCVQVKDRCAPVNSAFGFPWPDML 140
Qy 121 ECDRFPQDNDLCIPLASSDHLLPATEAPKVEACKNKNDNDIMETLCKNDFAIKVK 180
Db 141 ECDRFPQDNDLCIPLASSDHLLPATEAPKVEACKNKNDNDIMETLCKNDFAIKVK 200
Qy 181 KEITYINRDTKILLETKSTKIYKLVGVSERDLKKSILWLKDSLQCTCEEMNDINAPYLVM 240
Db 201 KEITYINRDTKILLETKSTKIYKLVGVSERDLKKSILWLKDSLQCTCEEMNDINAPYLVM 260
Qy 241 GQKQGGELVITSVKRWQKGOREPKRISRSIRKLQC 275
Db 261 GQKQGGELVITSVKRWQKGOREPKRISRSIRKLQC 295
RESULT 12
US-09-978-189-415
; Sequence 415, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavina, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR FILING DATE: 1998-03-11
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR APPLICATION NUMBER: 60/078886
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PRIOR APPLICATION NUMBER: 60/078939
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PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
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PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333

PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-01
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PRIOR FILING DATE: 1998-04-08
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PRIOR APPLICATION NUMBER: 60/082700
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PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
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PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.7%; Score 1483; DB 10; Length 295;
Best Local Similarity 99.6%; Pred. No. 2.4e-129;
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SARGLFPGQPDFSYKRSNCKPDPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60
Db |||||
Qy 21 SARGLFPGQPDFSYKRSNCKPDPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80
Db |||||
Qy 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQKRCAPVMSAFGFPWPDML 120
Db |||||
Qy 81 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQKRCAPVMSAFGFPWPDML 140
Db |||||
Qy 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCEACKNKNDNDNDIMETLCKNDFAKIKV 180
Db |||||
Qy 141 ECDRFPQNDLCIPLASSDHLPPATEAPKVCEACKNKNDNDNDIMETLCKNDFAKIKV 200
Db |||||
Qy 181 KEITYINRDTKIILLETKSTIYKLVGVSERDLKKSVLWLDKSLQCTCEMNDINAPYLVM 240
Db |||||
Qy 201 KEITYINRDTKIILLETKSTIYKLVGVSERDLKKSVLWLDKSLQCTCEMNDINAPYLVM 260
Db |||||
Qy 241 GQKGGELVITSVKRWQKGQREFKRISIRKLOC 275
Db |||||
Qy 261 GQKGGELVITSVKRWQKGQREFKRISIRKLOC 295
Db |||||

RESULT 13
US-09-978-608A-415
; Sequence 415, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kllavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 415
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-415

Query Match 99.7%; Score 1483; DB 10; Length 295;
Best Local Similarity 99.6%; Pred. No. 2.4e-129;
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SARGLFPGQPDFSYKRSNCKPDPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60
Db |||||
Qy 21 SARGLFPGQPDFSYKRSNCKPDPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80
Db |||||
Qy 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQKRCAPVMSAFGFPWPDML 120
Db |||||
Qy 81 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQKRCAPVMSAFGFPWPDML 140
Db |||||
Qy 121 ECDRFPQNDLCIPLASSDHLPPATEAPKVCEACKNKNDNDNDIMETLCKNDFAKIKV 180
Db |||||
Qy 141 ECDRFPQNDLCIPLASSDHLPPATEAPKVCEACKNKNDNDNDIMETLCKNDFAKIKV 200
Db |||||
Qy 181 KEITYINRDTKIILLETKSTIYKLVGVSERDLKKSVLWLDKSLQCTCEMNDINAPYLVM 240
Db |||||
Qy 201 KEITYINRDTKIILLETKSTIYKLVGVSERDLKKSVLWLDKSLQCTCEMNDINAPYLVM 260
Db |||||
Qy 241 GQKGGELVITSVKRWQKGQREFKRISIRKLOC 275
Db |||||
Qy 261 GQKGGELVITSVKRWQKGQREFKRISIRKLOC 295
Db |||||

RESULT 14
US-09-978-585A-415
; Sequence 415, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

PRIOR APPLICATION NUMBER: 60/080328	PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333	PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334	PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070	PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049	PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071	PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195	PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229	PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838	PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796	PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336	PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-06

:	PRIOR FILING DATE:	1998-05-07
:	PRIOR APPLICATION NUMBER:	60/084639
:	PRIOR FILING DATE:	1998-05-07
:	PRIOR APPLICATION NUMBER:	60/084640
:	PRIOR FILING DATE:	1998-05-07
:	PRIOR APPLICATION NUMBER:	60/084598
:	PRIOR FILING DATE:	1998-05-07
:	PRIOR APPLICATION NUMBER:	60/084600
:	PRIOR FILING DATE:	1998-05-07
:	PRIOR APPLICATION NUMBER:	60/084627
:	PRIOR FILING DATE:	1998-05-07
:	PRIOR APPLICATION NUMBER:	60/084643
:	PRIOR FILING DATE:	1998-05-07
:	PRIOR APPLICATION NUMBER:	60/085339
:	PRIOR FILING DATE:	1998-05-13
:	PRIOR APPLICATION NUMBER:	60/085338
:	PRIOR FILING DATE:	1998-05-13
:	PRIOR APPLICATION NUMBER:	60/085323
:	PRIOR FILING DATE:	1998-05-13
:	PRIOR APPLICATION NUMBER:	60/085582
:	PRIOR FILING DATE:	1998-05-15
:	PRIOR APPLICATION NUMBER:	60/085700
:	PRIOR FILING DATE:	1998-05-15
:	PRIOR APPLICATION NUMBER:	60/085689
:	PRIOR FILING DATE:	1998-05-15
:	PRIOR APPLICATION NUMBER:	60/085579
:	PRIOR FILING DATE:	1998-05-15
:	PRIOR APPLICATION NUMBER:	60/085580
:	PRIOR FILING DATE:	1998-05-15
:	PRIOR APPLICATION NUMBER:	60/085573
:	PRIOR FILING DATE:	1998-05-15
:	PRIOR APPLICATION NUMBER:	60/085704
:	PRIOR FILING DATE:	1998-05-15
:	PRIOR APPLICATION NUMBER:	60/085697

Query Match		99.7%;	Score 1483;	DB 10;	Length 295;
Best Local Similarity		99.6%;	Pred. No. 2.4e-129;		
Matches 274;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	SARGLFLFGQPDFSYSKRSNCKP	I	PANLQLCHGIEYQNMRLLPNLLGHETMKEVLEOAGAWI	60
Dd	21	SARGLFLFGQPDFSYSKRSNCKP	I	PNVLQLCHGIEYQNMRLLPNLLGHETMKEVLEOAGAWI	80
Qy	61	PLVMKQCHPDTKKFCLSLFAPVC	L	LDDETTIQPCHSLCVQVKDRCAPVMSAFGPFPDML	120
Dd	81	PLVMKQCHPDTKKFCLSLFAPVC	L	LDDETTIQPCHSLCVQVKDRCAPVMSAFGPFPDML	140
Qy	121	ECDRFPQDNDLCTPLASSDHLLP	A	TPEAPKVCEACKNKNDNDNDIMETLCKNDFALKTKV	180
Dd	141	ECDRFPQDNDLCTPLASSDHLLP	A	TPEAPKVCEACKNKNDNDNDIMETLCKNDFALKTKV	200
Qy	181	KEITYINRDKTIILETSKTYIKL	N	GVSRDLKKSVLWLKDSLOCTCEEMNDINAPYLVM	240
Dd	201	KEITYINRDKTIILETSKTYIKL	N	GVSRDLKKSVLWLKDSLOCTCEEMNDINAPYLVM	260
Qy	241	GQKGGLVITTSVKRWQVGOREFK	R	ISIRKLQC	275
Dd	261	GQKGGLVITTSVKRWQVGOREFK	R	ISIRKLQC	295

Search completed: September 1, 2005, 11:13:51
Job time : 108.105 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 10:25:34 ; Search time 29.4298 Seconds
(without alignments)
697.540 Million cell updates/sec

Title: US-08-949-904A-3

Perfect score: 1487

Sequence: 1 SARGULFGQDFSYKRSNC.....WKGQREFKRSIRKILQC 275

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/protdata/1/1aa/5A-COMB.pep:*
- 2: /cgn2_6/protdata/1/1aa/5B-COMB.pep:*
- 3: /cgn2_6/protdata/1/1aa/6A-COMB.pep:*
- 4: /cgn2_6/protdata/1/1aa/6B-COMB.pep:*
- 5: /cgn2_6/protdata/1/1aa/PTUS-COMB.pep:*
- 6: /cgn2_6/protdata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1479	99.5	295	4	US-09-148-545-179 Sequence 179, App
2	1479	98.5	296	4	US-09-148-545-237 Sequence 237, App
3	1474	99.1	295	4	US-08-937-067-2 Sequence 2, Appli
4	1033	69.5	212	4	US-08-937-067-4 Sequence 4, Appli
5	614	41.3	305	4	US-09-949-016-7706 Sequence 7706, Ap
6	614	41.3	317	4	US-08-937-067-6 Sequence 6, Appli
7	614	41.3	317	4	US-09-949-016-6300 Sequence 6300, Ap
8	602	40.5	313	4	US-09-546-043-3 Sequence 3, Appli
9	602	40.5	338	4	US-09-546-043-4 Sequence 4, Appli
10	600.5	40.4	313	4	US-09-514-885-1 Sequence 1, Appli
11	600.5	40.4	314	4	US-09-949-016-6299 Sequence 6299, Ap
12	600.5	40.4	314	4	US-08-937-067-7 Sequence 7, Appli
13	590	39.7	113	4	US-09-087-031E-24 Sequence 24, Appli
14	583.5	38.2	313	4	US-09-087-031E-4 Sequence 4, Appli
15	583.5	39.2	314	4	US-09-087-031E-3 Sequence 3, Appli
16	479	32.2	295	3	US-08-893-654B-6 Sequence 6, Appli
17	474	31.9	267	4	US-09-546-043-7 Sequence 7, Appli
18	455.5	30.6	246	4	US-09-546-043-6 Sequence 6, Appli
19	433.5	29.2	280	3	US-08-893-654B-4 Sequence 4, Appli
20	406.5	27.3	281	3	US-08-893-654B-2 Sequence 2, Appli
21	378	25.4	195	4	US-09-546-043-5 Sequence 5, Appli
22	353	23.7	109	4	US-09-087-031E-19 Sequence 19, Appli
23	275	18.5	685	4	US-08-937-067-14 Sequence 14, Appli
24	264.5	17.8	572	4	US-08-937-067-13 Sequence 13, Appli
25	264	17.8	537	4	US-08-937-067-11 Sequence 11, Appli
26	260.5	17.5	114	4	US-09-087-031E-15 Sequence 15, Appli
27	256.5	17.2	565	4	US-08-937-067-8 Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-148-545-179
; Sequence 179, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23

Sequence 9, Appli
Sequence 9, Appli
Sequence 479, App
Sequence 7544, Ap
Sequence 7, Appli
Sequence 3, Appli
Sequence 10, Appli
Sequence 8, Appli
Sequence 21, Appli
Sequence 12, Appli
Sequence 20, Appli
Sequence 17, Appli
Sequence 14, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 16, Appli
Sequence 10, Appli


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; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 295

Query Match          99.5%; Score 1479; DB 4; Length 295;
Best Local Similarity 99.3%; Pred. No. 2.8e-154;
Matches 273; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SARGFLFGQPDFSKYKRNCKDIPANLQICHGIEYQNRMLPNLLGHETMKVEVLEQAGAWI 60
   |||||
Db 21 SARGFLFGQPDFSKYKRNCKDIPYNLQICHGIEYQNRMLPNLLGHETMKVEVLEQAGAWI 80
   |||||
QY 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLBETIQPCHSLCVQVKDRCAPVMSAFGFFWPDML 120
   |||||
Db 81 PLVMKQCHPDTKKFLCSLFAFVCLDDLBETIQPCHSLCVQVKDRCAPVMSAFGFFWPDML 140
   |||||
QY 121 ECDRFPQNDLCIPLASSDHLPLATEAPKVCEACKNNKDDDDIMETLCKNDFALKIKV 180
   |||||
Db 141 ECDRFPQNDLCIPLASSDHLPLATEAPKVCEACKNNKDDDDIMETLCKNDFALKIKV 200
   |||||
QY 181 KEITYINRDTKIILTKSTKIYKLVGVSERDLKKSVLWLNKDSLOCTCEBMDINAPYLV 240
   |||||
Db 201 KEITYINRDTKIILTKSTKIYKLVGVSERDLKKSVLWLNKDSLOCTCEBMDINAPYLV 260
   |||||
QY 241 GOKQGGELVITSVKRWQKGQREFKRISIRKLOC 275
   |||||
Db 261 GOKQGGELVITSVKRWQKGQREFKRISIRKLOC 295
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RESULT 2

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US-09-148-545-237
; Sequence 237, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001PI
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
```

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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
```


TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-937-067-2

Query Match
Best Local Similarity 99.1%; Score 1474; DB 4; Length 295;
Matches 272; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60
21 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80
61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTQPCHSCLCVQVKDRCAPVMSAFGFPWDM 120
81 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTQPCHSCLCVQVKDRCAPVMSAFGFPWDM 140
121 ECDRFPQNDLCIPLASSDHLPLATEAPKVCACKNKDDNDIMETLCKNDPALKIKV 180
141 ECDRFPQNDLCIPLASSDHLPLATEAPKVCACKNKDDNDIMETLCKNDPALKIKV 200
181 KEITYINRDTKIIETKSKTIYKLVNGVSRDLKKSVMWKSLQCTCEEMNDINAPYLVM 240
201 KEITYINRDTKIIETKSKTIYKLVNGVSRDLKKSVMWKSLQCTCEEMNDINAPYLVM 260
241 GOKQGGELVITSVKRWQKQREFFKRSIRSLKQC 275
261 GOKQGGELVITSVKRWQKQREFFKRSIRSLKQC 295

RESULT 4
US-08-937-067-4
Sequence 4, Application US/08937067.
Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Unanaky, Samuil
APPLICANT: Meikonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-937-067-4

Query Match
Best Local Similarity 69.5%; Score 1033; DB 4; Length 212;
Matches 187; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60
21 SARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80
61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTQPCHSCLCVQVKDRCAPVMSAFGFPWDM 120
81 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTQPCHSCLCVQVKDRCAPVMSAFGFPWDM 140
121 ECDRFPQNDLCIPLASSDHLPLATEAPKVCACKNKDDNDIMETLCKNDPALKIKV 180
141 ECDRFPQNDLCIPLASSDHLPLATEAPKVCACKNKDDNDIMETLCKNDPALKIKV 200
181 KEITYINR 188
201 KEITYINR 208

RESULT 5
US-09-949-016-7706
Sequence 7706, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7706
LENGTH: 305
TYPE: PRT
ORGANISM: Human
US-09-949-016-7706

Query Match
Best Local Similarity 41.3%; Score 614; DB 4; Length 305;
Matches 119; Conservative 46; Mismatches 78; Indels 12; Gaps 6;

14 SY-KRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTK 72
34 SYSKPPQCLDIPADLPCHTGVYKRMRLPNLLEHSAEVKQASSMLPLAKRCHSDTQ 93
73 KFLCSLFAFVCLDDLDDETTQPCHSCLCVQVKDRCAPVMSAFGFPWDMLECDRFPQNDLC 132
94 VFLCSLFAFVCLDDLDDETTQPCHSCLCVQVKDRCAPVMSAFGFPWDMLECDRFPQNDLC 150
133 IPLASSDHLPLATEAPKVCACKNKDDNDIMETLCKNDPALKIKVKEITYINR 189
151 IAVQFGH--LPAT--APPVTKICACEMHSADG-LMEQMCSSDFVVKRRIKEIKENG 205
190 TKIILETKSKTIYKLVNGVSRDLKKSVMWKSLQCTCEEMNDINAPYLVMGKQGGELV 249
206 RKLIGAQKKKLLKPGPLKRDTRKLVLMKNGAGCCPQLDSLAGSLVNGRKVDGQLL 265
250 ITSVMKQKQREFFK 264
266 LMAVTRWDKKKEMK 280

RESULT 6
US-08-937-067-6
; Sequence 6, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-067-6

Query Match 41.3%; Score 614; DB 4; Length 317;
Best Local Similarity 46.7%; Pred. No. 5.4e-59;
Matches 119; Conservative 46; Mismatches 78; Indels 12; Gaps 6;

QY 14 SY-KRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTK 72
DB 46 SYSKPPQCLDIPADLPCHTVGYKRMRLPNLLEHESLAEVKQQAASSWLPPLAKRCHSDTQ 105
QY 73 KFLCSLFPAPVCLDDLDLTIQPCHSICVQVKRCAPVMSAFGPPWPMLECDRFPQDNDLC 132
DB 106 VFCLSLFAPVC--LDRPIYPCSLCEAVRACAPLMEAYGFPWPEMLHCHKFPDLNDLC 162
QY 133 IPLASDHLLPATEAP---KVCEACKNKNDDNDIMETLCKNDPALKIKVKEITYINRD 189
DB 163 IAVQFGH--LPAT--APPVTKICACEMEHSADG-LMEQMCSSDFVVKMKRIKEIKIENG 217
QY 190 TKIILETSKTIYKLVNGVSRDLKSVLWLDLSLOCTCEEMNDINAPVLVWGKOGGELV 249
DB 218 RKLGAQKKKKLPGPKRKTDLVLMKNAGAGCCPQLDSLGSFLVMGRKVDGQLL 277
QY 250 ITSVKRWKQGREFK 264
DB 278 LMAVYRWKKNKEMK 292

RESULT 7
US-09-949-016-6300
; Sequence 6300, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6300
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6300

Query Match 41.3%; Score 614; DB 4; Length 317;
Best Local Similarity 46.7%; Pred. No. 5.4e-59;
Matches 119; Conservative 46; Mismatches 78; Indels 12; Gaps 6;

QY 14 SY-KRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTK 72
DB 46 SYSKPPQCLDIPADLPCHTVGYKRMRLPNLLEHESLAEVKQQAASSWLPPLAKRCHSDTQ 105
QY 73 KFLCSLFPAPVCLDDLDLTIQPCHSICVQVKRCAPVMSAFGPPWPMLECDRFPQDNDLC 132
DB 106 VFCLSLFAPVC--LDRPIYPCSLCEAVRACAPLMEAYGFPWPEMLHCHKFPDLNDLC 162
QY 133 IPLASDHLLPATEAP---KVCEACKNKNDDNDIMETLCKNDPALKIKVKEITYINRD 189
DB 163 IAVQFGH--LPAT--APPVTKICACEMEHSADG-LMEQMCSSDFVVKMKRIKEIKIENG 217
QY 190 TKIILETSKTIYKLVNGVSRDLKSVLWLDLSLOCTCEEMNDINAPVLVWGKOGGELV 249
DB 218 RKLGAQKKKKLPGPKRKTDLVLMKNAGAGCCPQLDSLGSFLVMGRKVDGQLL 277
QY 250 ITSVKRWKQGREFK 264
DB 278 LMAVYRWKKNKEMK 292

RESULT 8
US-09-546-043-3
; Sequence 3, Application US/09546043
; Patent No. 6600018
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffery et al.,
; TITLE OF INVENTION: SECRETED FRIZZLED RELATED PROTEIN, SFRP, FRAGMENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 53990
; CURRENT APPLICATION NUMBER: US/09/546,043
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-043-3

Query Match 40.5%; Score 602; DB 4; Length 313;
Best Local Similarity 41.0%; Pred. No. 1.1e-57;
Matches 118; Conservative 56; Mismatches 94; Indels 20; Gaps 6;

QY 1 SARGL-----FLFGQPD-----FSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHE 47
DB 25 SGRGLGSEYDVVSFQSDIGPYQSGRFYTKPPQCVDPADLRLCHNVGKVMKVLNLLSHE 84

QY 48 TMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAP 107
Db 85 TMAEVKQOASSWVPLLNKNCHAGTQVFLCSLPAPVC---LDRPIYPCRWLCEAVRDSCEP 141
QY 108 VMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLLPATEAPKVCCEACKNKNDNDIME 167
Db 142 VMQFFGYWPEMLKCDKFP-EGDVCIAMTPPNATEASKPGQTTVCPPCDNELKSE-AIIE 199
QY 168 TLCKNDPALKIKVEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLKDSLQCTC 227
Db 200 HLCASEFALRMKIKEVKGKNGDKIV--PKKKPLKLGPIKKDLKLVLYLKNKGADCP 257
QY 228 EEMNDINAPYLVMGQKQSGELVITSVKRWKQKOREFKRISRSIRKLQOC 275
Db 258 HQLDNLSSHFLINGRKVKYSQYLLTAIHKWDKKNKEFKFMKKNHEC 305

RESULT 9

US-09-546-043-4
; Sequence 4, Application US/09546043
; Patent No. 6600018
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffery et al.,
; TITLE OF INVENTION: SECRETED FRIZZLED RELATED PROTEIN, sFRP, FRAGMENTS AND
; FILE REFERENCE: 53990
; CURRENT APPLICATION NUMBER: US/09/546,043
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-043-4

Query Match 40.5%; Score 602; DB 4; Length 338;
Best Local Similarity 41.0%; Pred. No. 1.2e-57;
Matches 118; Conservative 56; Mismatches 94; Indels 20; Gaps 6;

QY 1 SARGL-----FLFGQPD-----PSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHE 47
Db 25 SGRGLSEYDYVSFOSDIPGYSGREYTKPPQCVDPADLRLCHNVGYKQWLPNLLHE 84
QY 48 TMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAP 107
Db 85 TMAEVKQOASSWVPLLNKNCHAGTQVFLCSLPAPVC---LDRPIYPCRWLCEAVRDSCEP 141
QY 108 VMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLLPATEAPKVCCEACKNKNDNDIME 167
Db 142 VMQFFGYWPEMLKCDKFP-EGDVCIAMTPPNATEASKPGQTTVCPPCDNELKSE-AIIE 199
QY 168 TLCKNDPALKIKVEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLKDSLQCTC 227
Db 200 HLCASEFALRMKIKEVKGKNGDKIV--PKKKPLKLGPIKKDLKLVLYLKNKGADCP 257
QY 228 EEMNDINAPYLVMGQKQSGELVITSVKRWKQKOREFKRISRSIRKLQOC 275
Db 258 HQLDNLSSHFLINGRKVKYSQYLLTAIHKWDKKNKEFKFMKKNHEC 305

RESULT 10

US-09-514-885-1
; Sequence 1, Application US/09514885
; Patent No. 6656461
; GENERAL INFORMATION:
; APPLICANT: D'Armiento, Jeanine
; APPLICANT: Imai, Kazuishi
; TITLE OF INVENTION: NOVEL THERAPEUTIC TREATMENT OF CHRONIC OBSTRUCTIVE
; FILE REFERENCE: 58483.app
; CURRENT APPLICATION NUMBER: US/09/514,885
; CURRENT FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Human
US-09-514-885-1

Query Match 40.4%; Score 600.5; DB 4; Length 313;
Best Local Similarity 42.6%; Pred. No. 1.6e-57;
Matches 112; Conservative 54; Mismatches 90; Indels 7; Gaps 4;

QY 13 PSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHEITMKEVLEQAGAWIPLVMKQCHPDTK 72
Db 50 FYTKPPQCVDPADLRLCHNVGYKQWLPNLLHEITMAEVKQOASSWVPLLNKNCHAGTQ 109
QY 73 KFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAPVMSAFGFPWDMLECDRFPQDNDLC 132
Db 110 VFLCSLPAPVC---LDRPIYPCRWLCEAVRDSCEPVMQFFGYWPEMLKCDKFP-EGDVC 165
QY 133 IPLASSDHLLPATEAPKVCCEACKNKNDNDIMETLCKNDPALKIKVEITYINRDTKI 192
Db 166 IAMTPPNATEASKPGQTTVCPPCDNELKSE-AIIEHLCASEFALRMKIKEVKGKNGDKKI 224
QY 193 ILETKSTIYKLVGVSERDLKKSVMWLKDSLQCTCEEMNDINAPYLVMGQKQSGELVITS 252
Db 225 V--PKKKPLKLGPIKKDLKLVLYLKNKGADCPCHQDNLSSHFLINGRKVKYSQYLLTA 282
QY 253 VKRWKQKOREFKRISRSIRKLQOC 275
Db 283 IHKWDKKNKEFKFMKKNHEC 305

RESULT 11

US-09-949-016-6299
; Sequence 6299, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6299
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6299

Query Match 40.4%; Score 600.5; DB 4; Length 313;
Best Local Similarity 42.6%; Pred. No. 1.6e-57;
Matches 112; Conservative 54; Mismatches 90; Indels 7; Gaps 4;

QY 13 PSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHEITMKEVLEQAGAWIPLVMKQCHPDTK 72
Db 50 FYTKPPQCVDPADLRLCHNVGYKQWLPNLLHEITMAEVKQOASSWVPLLNKNCHAGTQ 109
QY 73 KFLCSLPAPVCLDLDLDETIQCHSLCVQVKDRCAPVMSAFGFPWDMLECDRFPQDNDLC 132
Db 110 VFLCSLPAPVC---LDRPIYPCRWLCEAVRDSCEPVMQFFGYWPEMLKCDKFP-EGDVC 165
QY 133 IPLASSDHLLPATEAPKVCCEACKNKNDNDIMETLCKNDPALKIKVEITYINRDTKI 192
Db 166 IAMTPPNATEASKPGQTTVCPPCDNELKSE-AIIEHLCASEFALRMKIKEVKGKNGDKKI 224


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Db 45 YGSGRFYTKPPGCVDPADLR LCHNVGYKQWLPNLLEHETWAEVKGASSWVPLLNKNC 104
Qy 68 HPDTKKFLCSLPAPVCLDLDLDTIQCHSLCVQVKDRCAPVMSAFGFPWPDMLECDRFPQ 127
Db 105 HAGTGVFLCSLPAPVC---LDRPIYFCRWLCEAVRDSCEPVMGFFGYWPEMLKCDKFP- 160
Qy 128 DNDLCIPLASSDHLPLATEAPK-----VCEACKNKDDNDIMETLCKNDFAIKIKVKE 182
Db 161 EGDVCIAMTP-----PNATEASKPGGTTVCPDCDNLKSE-AIIHLCASEFALRWKIKE 214
Qy 183 ITYINRDTKIILETKSTIYKLVGSEDLKKSVLWLDLSLOCTCEEMNDINAPYLVMQO 242
Db 215 VKKENGDKKIV--PKKKPLKLGPIKKDKLKKLVLYLKNAGADCPCHGLDNLSHHFLIMGR 272
Qy 243 KGGELVITSVKRWKQKQREFKRISIRKLOC 275
Db 273 KVKSGYLLTAIHKWDKKNKEFNFMKMKKNHEC 305

RESULT 15
US-09-087-031E-3
; Sequence 3, Application US/09087031E
; Patent No. 6479255
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
; FILE REFERENCE: 11613.13US11
; CURRENT APPLICATION NUMBER: US/09/087,031E
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/087,031
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/050,417
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-087-031E-3

Query Match 39.2%; Score 583.5; DB 4; Length 314;
Best Local Similarity 42.5%; Pred. No. 1.2e-55;
Matches 116; Conservative 48; Mismatches 92; Indels 17; Gaps 6;

Qy 8 FQOPDFSFKRSCKPIPANLQLCHGIEYQNMRLPNLLGHETMKEVLEQAGAWIPLVMKQC 67
Db 46 YGSGRFYTKPPGCVDPADLR LCHNVGYKQWLPNLLEHETWAEVKGASSWVPLLNKNC 105
Qy 68 HPDTKKFLCSLPAPVCLDLDLDTIQCHSLCVQVKDRCAPVMSAFGFPWPDMLECDRFPQ 127
Db 106 HAGTGVFLCSLPAPVC---LDRPIYFCRWLCEAVRDSCEPVMGFFGYWPEMLKCDKFP- 161
Qy 128 DNDLCIPLASSDHLPLATEAPK-----VCEACKNKDDNDIMETLCKNDFAIKIKVKE 182
Db 162 EGDVCIAMTP-----PNATEASKPGGTTVCPDCDNLKSE-AIIHLCASEFALRWKIKE 215
Qy 183 ITYINRDTKIILETKSTIYKLVGSEDLKKSVLWLDLSLOCTCEEMNDINAPYLVMQO 242
Db 216 VKKENGDKKIV--PKKKPLKLGPIKKDKLKKLVLYLKNAGADCPCHGLDNLSHHFLIMGR 273
Qy 243 KGGELVITSVKRWKQKQREFKRISIRKLOC 275
Db 274 KVKSGYLLTAIHKWDKKNKEFNFMKMKKNHEC 306
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Search completed: September 1, 2005, 10:56:28
Job time : 30.4298 secs

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OM protein - protein search, using sw model

Run on: September 1, 2005, 09:41:17 ; Search time 112.412 Seconds
(without alignments)
946.152 Million cell updates/sec

Title: US-08-949-904A-3

Perfect score: 1487

Sequence: 1 SARGLFLRGQDPFSYKRSNC.....WQKGQREPKRISIRKLQC 275

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980a:*
- 2: Geneseq1990a:*
- 3: Geneseq2000a:*
- 4: Geneseq2001a:*
- 5: Geneseq2002a:*
- 6: Geneseq2003a:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1487	100.0	275	7	Adf77694 Human mat
2	1487	100.0	295	2	Aaw82588 Human ATG
3	1487	100.0	295	2	Aaw49082 Homo sapi
4	1487	100.0	295	2	Aay06923 Human sec
5	1487	100.0	295	5	Abg31499 Human sec
6	1487	100.0	295	6	Abu55908 Human pro
7	1487	100.0	295	6	Aac34062 SARP 2 pr
8	1487	100.0	295	6	Abx47455 Breast Ca
9	1487	100.0	295	7	Adf77693 Human ful
10	1487	100.0	295	7	Adn40027 Cancer/an
11	1487	100.0	295	8	Adn05090 Antipsori
12	1487	100.0	295	8	Adr46694 Cancer-as
13	1483	99.7	295	2	Aay41748 Human PRO
14	1483	99.7	295	3	Aab44304 Human PRO
15	1483	99.7	295	5	Abb84861 Human PRO
16	1483	99.7	295	5	Abb95467 Human ang
17	1483	99.7	295	6	Abu25250 Novel hum
18	1483	99.7	295	6	Abu72256 Novel hum
19	1483	99.7	295	6	Abu84936 Human sec
20	1483	99.7	295	6	Abu61134 Human PRO
21	1483	99.7	295	6	Abu80403 Human sec
22	1483	99.7	295	6	Adr424954 Novel hum
23	1483	99.7	295	6	Abu19705 Novel hum
24	1483	99.7	295	6	Ada12615 Human sec
25	1483	99.7	295	6	Abu19596 Novel hum

26	1483	99.7	295	7	ADB73921 Human PRO
27	1483	99.7	295	7	ADB76637 Human PRO
28	1483	99.7	295	7	Adc44063 Human sec
29	1483	99.7	295	7	Adc61823 Human sec
30	1483	99.7	295	7	Adc63787 Human sec
31	1483	99.7	295	7	Adc66887 Human sec
32	1483	99.7	295	7	Adc69011 Human sec
33	1483	99.7	295	7	Adc63071 Human sec
34	1483	99.7	295	7	Adc68136 Human sec
35	1483	99.7	295	7	Adc41456 Human sec
36	1483	99.7	295	7	Adc67511 Human sec
37	1483	99.7	295	7	Adc62447 Human sec
38	1483	99.7	295	7	Adc42080 Human sec
39	1483	99.7	295	7	Adc10379 Human sec
40	1483	99.7	295	7	Adc11339 Human sec
41	1483	99.7	295	7	Adc37132 Human sec
42	1483	99.7	295	7	Adc49449 Human sec
43	1483	99.7	295	7	Adc35503 Human sec
44	1483	99.7	295	7	Adc16617 Human sec
45	1483	99.7	295	7	Adc73232 Human sec

ALIGNMENTS

RESULT 1
ADf77694
ID ADf77694 standard; protein; 275 AA.
XX AC ADf77694;
XX DT 26-FEB-2004 (first entry)

DE Human mature Frazzled family protein SDF-5.

XX KW Human; Frazzled family protein; SDF-5; pancreatic gene; chondrocyte differentiation; cartilage tissue formation; tissue repair; pancreatic tissue repair; cartilage disorders; osteoarthritis; rheumatoid arthritis; articular cartilage defect; nutritional source; nutritional supplement; immune deficiency; infection; HIV infection; hepatitis; cancer; diabetes; inflammation; asthma; neurological disorder; Parkinson's disease; Alzheimer's disease; Huntington's disease.
XX OS Homo sapiens.
XX PN US2003175855-A1.
XX PD 18-SEP-2003.
XX PF 15-OCT-1997; 97US-00949904.
XX PR 06-FEB-1997; 97US-00796153.
XX PR 08-MAY-1997; 97US-00848439.
XX PA (LAVA)/ LAVALLIE E R.
XX PI (RACI)/ RACIE L A.
XX PI Lavallie ER, Racie LA;
XX DR WPI; 2003-898533/82.
XX PS N-PSDB; ADf77692.
XX PT New human SDF-5 DNA, useful for inducing formation, growth, differentiation, proliferation or maintenance of chondrocytes or cartilage tissues, or as nutritional sources or supplements.
XX PS Claim 18; SEQ ID NO 3; 24pp; English.
XX CC The invention relates to an isolated DNA sequence encoding mature or full length human SDF-5 (a frazzled family member) or its defined fragments, or which hybridises to it under stringent hybridisation conditions and encodes a protein that exhibits Frazzled activity. Also included are a vector comprising the above DNA molecule in operative association with an

CC expression control sequence, a host cell transformed with the vector, a
 CC method for producing purified human SDF-5 protein, a purified human SDF-5
 CC polypeptide, a composition comprising a therapeutic amount of at least
 CC one human SDF-5 polypeptide cited above, a method for altering the
 CC regulation of pancreatic genes in a patient (comprising administering to
 CC the patient an amount of the composition cited above), antibodies to a
 CC purified human SDF-5 protein and a method for increasing the
 CC differentiation of cells into chondrocytes, comprising applying a
 CC composition comprising BMP-2 (bone morphogenetic protein-2) and SDF-5.
 CC The DNA and protein are useful in regulating the binding of Wnt (wingnut)
 CC genes to their receptor or in inducing formation, growth,
 CC differentiation, proliferation and/or maintenance of chondrocytes and/or
 CC cartilage tissue, and for other tissue repair, such as pancreatic tissue
 CC repair. These may be used in the treatment of cartilage disorders, such
 CC as osteoarthritis, rheumatoid arthritis or articular cartilage defects.
 CC These may also be used for augmenting the activity of other tissue
 CC regenerating and differentiation factors. In addition, the protein and
 CC DNA are used as nutritional sources or supplements and in treating
 CC various immune deficiencies and disorders (e.g. infections, HIV,
 CC hepatitis, cancer, diabetes, inflammation or asthma) or neurological
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease or Huntington's
 CC disease). The present sequence represents mature human SDF-5.

XX Sequence 275 AA;

Query Match 100.0%; Score 1487; DB 7; Length 275;
 Best Local Similarity 100.0%; Pred. No. 5.8e-138;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKVELEAGAWI 60
 DB 1 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKVELEAGAWI 60
 QY 61 PLVMKQCHPDPTKFLCSLFAFVCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 120
 DB 61 PLVMKQCHPDPTKFLCSLFAFVCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 120
 QY 121 ECDRFPQDNDLCIPLASSDHLLPATEAPKVCYCKNKNDDNDIMETLCRNDFAKIKV 180
 DB 121 ECDRFPQDNDLCIPLASSDHLLPATEAPKVCYCKNKNDDNDIMETLCRNDFAKIKV 180
 QY 181 KEITYINRDTKIILETSKTIYKLVGVSERDLKKSVMWKDSLOQTCCEMNDINAPYLV 240
 DB 181 KEITYINRDTKIILETSKTIYKLVGVSERDLKKSVMWKDSLOQTCCEMNDINAPYLV 240
 QY 241 GQKGGELVITSVKRWQKGQREFKRISRSIRKLQ 275
 DB 241 GQKGGELVITSVKRWQKGQREFKRISRSIRKLQ 275

RESULT 2

AAW82588
 ID AAW82588 standard; protein; 295 AA.

AC AAW82588;

XX 01-MAR-1999 (first entry)

DE Human ATG-1622 protein.

KW ATG-1622; SDF5; human; secreted ligand; 7-transmembrane receptor;
 KW diagnosis; disease; screening; vaccine; inoculate; treatment; obesity;
 KW heart disease; hypertension; kidney diseases; insulin resistance;
 KW lipodystrophy; diabetes; central nervous system; CNS; gene mapping;
 KW linkage analysis.

OS Homo sapiens.

PN EP879887-A1.

XX 25-NOV-1998.

PF 14-MAY-1998; 98EP-00303809.

XX 21-MAY-1997; 97US-0047251P.
 PR 13-JUN-1997; 97US-00874156.
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Hu E, Zhu Y;
 XX WPI; 1998-596879/51.
 DR N-PSDB; AAV69384.
 XX New human secreted protein ATG-1622 polypeptide and polynucleotide -
 XX useful as diagnostic reagents and for prevention and treatment of Central
 XX Nervous System diseases and diabetes.

PS Claim 11; Page 22-23; 28pp; English.

XX This sequence represents the human ATG-1622 protein which is related to
 CC human secreted ligands for 7-transmembrane receptors and similar to
 CC murine SDF5. ATG-1622 polypeptides and polynucleotides are useful for
 CC diagnosing susceptibility to diseases by detecting mutations in the ATG-
 CC 1622 gene and can diagnose diseases associated with ATG-1622 imbalance.
 CC The polypeptides can be used to screen for agonists and antagonists which
 CC can be used in treatment to activate or inhibit ATG-1622 activity. The
 CC ATG-1622 polypeptide can be administered directly or as a vaccine to
 CC inoculate against disease. Diseases which can be diagnosed, prevented or
 CC treated by the ATG-1622 polypeptide or polynucleotides include heart
 CC disease, hypertension, kidney diseases, obesity, insulin resistance,
 CC lipodystrophy, diabetes and central nervous system (CNS) diseases. The
 CC ATG-1622 polypeptide is also useful for mapping the gene to a chromosome,
 CC allowing gene inheritance to be studied through linkage analysis

XX Sequence 295 AA;

Query Match 100.0%; Score 1487; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 6.4e-138;
 Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKVELEAGAWI 60
 DB 21 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKVELEAGAWI 80
 QY 61 PLVMKQCHPDPTKFLCSLFAFVCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 120
 DB 81 PLVMKQCHPDPTKFLCSLFAFVCLDDLDDETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 140
 QY 121 ECDRFPQDNDLCIPLASSDHLLPATEAPKVCYCKNKNDDNDIMETLCRNDFAKIKV 180
 DB 141 ECDRFPQDNDLCIPLASSDHLLPATEAPKVCYCKNKNDDNDIMETLCRNDFAKIKV 200
 QY 181 KEITYINRDTKIILETSKTIYKLVGVSERDLKKSVMWKDSLOQTCCEMNDINAPYLV 240
 DB 201 KEITYINRDTKIILETSKTIYKLVGVSERDLKKSVMWKDSLOQTCCEMNDINAPYLV 260
 QY 241 GQKGGELVITSVKRWQKGQREFKRISRSIRKLQ 275
 DB 261 GQKGGELVITSVKRWQKGQREFKRISRSIRKLQ 295

RESULT 3

AAW49082
 ID AAW49082 standard; protein; 295 AA.

XX AAW49082;

XX 09-NOV-1998 (first entry)

XX Homo sapiens SDF-5 protein.

XX SDF-5; frazzled; osteoarthritis; rheumatoid arthritis; cell formation;
 KW proliferation; differentiation; diabetes; pancreatic cancer;
 KW wound healing; gene therapy.

XX	25-MAR-2002; 2002WO-GB0001195.	QY	61	PLVMKQCHPDTKKFLCSLFAFVCLDDLDLDTIQPCHSLCVQVKDRCAPVMSAFGFWPDM	120
XX	23-MAR-2001; 2001GB-00007296.	Db	81	PLVMKQCHPDTKKFLCSLFAFVCLDDLDLDTIQPCHSLCVQVKDRCAPVMSAFGFWPDM	140
PR	23-MAR-2001; 2001GB-00007299.	QY	121	ECDRPQNDLCIPLASSDHLHPATEAPKVCCEACKNNKDDDDNDIMETLCKNDFAKIKV	180
PR	17-APR-2001; 2001GB-00009346.	Db	141	ECDRPQNDLCIPLASSDHLHPATEAPKVCCEACKNNKDDDDNDIMETLCKNDFAKIKV	200
XX	(AXOR-) AXORDIA LTD.	QY	181	KEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWLDKSLQCTCEMNDINAPYLV	240
PI	Andrews P, Walsh J, Gokhale P;	Db	201	KEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWLDKSLQCTCEMNDINAPYLV	260
DR	WPI: 2003-092952/08.	QY	241	GQKQGGELVITSVKRWQKQREFKRISRSIRKLOC	275
DR	N-PSDB; ABX75335.	Db	261	GQKQGGELVITSVKRWQKQREFKRISRSIRKLOC	295
XX	Modulating the differentiation of embryonic stem cells by providing	RESULT 7			
PT	ligands which bind receptors in the Notch and Wnt pathways, useful for	AAE34062			
PT	treating diseases such as Parkinson's, Huntington's, heart disease,	ID	AAE34062	standard; protein; 295 AA.	
PT	diabetes and AIDS.	XX	AC	AAE34062;	
XX	Disclosure; Fig 82; 12lpp; English.	XX	DT	02-MAY-2003 (first entry)	
XX	The invention relates to modulating the differentiation of an embryonic	XX	DE	SARP 2 protein.	
CC	stem cell, comprising: (a) providing a culture of embryonic stem cells;	XX	KW	Drug screening; toxicology assay; signalling pathway; SARP 2.	
CC	(b) providing at least one ligand or its active binding fragment, capable	XX	OS	Unidentified.	
CC	of binding its cognate receptor polypeptide expressed by the embryonic	XX	PN	WO200290992-A2.	
CC	stem cell; (c) forming a culture comprising embryonic stem cells and the	XX	PD	14-NOV-2002.	
CC	ligand; and (d) growing the cell culture. Also included are: (i)	XX	PF	29-APR-2002; 2002WO-GB001946.	
CC	Modulating the differentiation of embryonic stem cells, comprising: (a)	XX	PR	04-MAY-2001; 2001GB-00011004.	
CC	providing a cell transfected with a nucleic acid molecule selected from:	XX	PA	(AXOR-) AXORDIA LTD.	
CC	(i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic	XX	PI	Andrews P, Draper J, Walsh J;	
CC	acid molecule that hybridises to the nucleic acid in (i), and which	XX	DR	WPI; 2003-120579/11.	
CC	encodes a ligand capable of modulating embryonic stem cell	XX	DR	N-PSDB; AAD52560.	
CC	differentiation, or capable of binding a Wnt receptor; or (iii) nucleic	XX	PT	Identifying biologically active agents comprises cloning transfected	
CC	acid molecules which are degenerate as a result of the genetic code to	XX	PT	cells into a cell array, exposing the array to an agent to be tested, and	
CC	the sequences of (i) or (ii); (b) forming a culture comprising the cell	XX	PT	detecting signals generated by a reporter molecule as a result of	
CC	identified in (a) with an embryonic stem cell; and (c) growing the	XX	XX	exposure to the agent.	
CC	cell; (2) inhibiting the differentiation of embryonic stem cells,	XX	PS	Claim 16; Fig 76; 90pp; English.	
CC	comprising: (a) providing at least one polypeptide or its active	XX	CC	The present invention relates to a novel screening method which enables	
CC	fragment, that are inhibitors of the Wnt signalling pathway; (b) forming	XX	CC	the identification of biologically active agents which mediate their	
CC	a culture comprising the cell identified in (a) with an embryonic stem	XX	CC	effect through the activation of genes. The method involves providing a	
CC	cell; and (c) growing the culture for the maintenance of embryonic stem	XX	CC	population of cells stably transfected with a nucleic acid encoding a	
CC	cells in an undifferentiated state; or (3) inhibiting the differentiation	XX	CC	reporter molecule, cloning the transfected cells into a cell array,	
CC	of embryonic stem cells, comprising: (a) providing a cell transfected	XX	CC	exposing the array to at least one agent to be tested and detecting a	
CC	with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt	XX	CC	signal generated by the reporter molecule as a result of exposure to the	
CC	inhibitory polypeptide; (ii) a molecule which hybridises to the molecule	XX	CC	agent. The method is useful in identifying biologically active agents and	
CC	of (i) and encodes a polypeptide capable of inhibiting Wnt signalling;	XX	CC	the genes through which the agents act, in screening potential drugs for	
CC	and (ii) nucleic acid molecules which are degenerate as a result of the	XX	CC	their ability to activate certain drug targets in a high-throughput	
CC	genetic code to the sequences of (i) or (ii); (b) forming a culture	XX	CC	assay, in identifying relationships between signalling pathways and	
CC	comprising the cell identified in (a) with an embryonic stem cell; and	XX	CC	specific signals that could be useful in eventually directing the	
CC	(c) growing the culture for the maintenance of embryonic stem cells in an	XX	CC	differentiation of embryonic stem cells and in toxicology assays by	
CC	undifferentiated state; and (4) A cell, therapeutic cell or cell culture	XX	CC	testing for unwanted activation or inhibition of specific signalling	
CC	obtainable by any of the methods cited above. The therapeutic cell of the	XX	CC	pathways. The present sequence is SARP 2 protein used to illustrate the	
CC	present invention is useful in the treatment of an animal, preferably a	XX	XX	method of the invention	
CC	human, comprising administering a cell composition comprising embryonic	XX	SQ	Sequence 295 AA;	
CC	stem cells which have been induced to differentiate into at least one				
CC	cell-type. The cell is also useful for the manufacture of a composition				
CC	for use in treatment of diseases such as Parkinson's disease,				
CC	Huntington's disease, motor neuron disease, heart disease, diabetes,				
CC	liver disease (e.g. cirrhosis), renal disease and AIDS (acquired				
CC	immunodeficiency syndrome). The present sequence is represents a Wnt or				
CC	Notch pathway protein (i.e. a ligand for the method of the invention)				
XX	Sequence 295 AA;				
SQ					
Query Match	100.0%; Score 1487; DB 6; Length 295;				
Best Local Similarity	100.0%; Pred. No. 6.4e-138;				
Matches 275; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
Query	1 SARGLFLGQPDFSVKRSNCKPDPANLQCHGIEYQNNRPLNLLGHETMKEVLEQAGAWI 50				
Db	21 SARGLFLGQPDFSVKRSNCKPDPANLQCHGIEYQNNRPLNLLGHETMKEVLEQAGAWI 80				

Query Match 100.0%; Score 1487; DB 6; Length 295;

FT XX /note= "Claimed in claim 2"
PN US2003175855-A1.
XX 18-SEP-2003.
XX 15-OCT-1997; 97US-00949904.
XX 06-FEB-1997; 97US-00796153.
PR 08-MAY-1997; 97US-00848439.
XX (LAVA/) LAVALLIE E R.
PA (RACI/) RACIE L A.
XX Lavallie ER, Racie LA;
XX WPI: 2003-898533/82.
DR N-PSDB; ADF77692.
XX New human SDF-5 DNA, useful for inducing formation, growth,
PT differentiation, proliferation or maintenance of chondrocytes or
PT cartilage tissues, or as nutritional sources or supplements.
XX Claim 18; SEQ ID NO 2; 24pp; English.
XX The invention relates to an isolated DNA sequence encoding mature or full
CC length human SDF-5 (a frazzled family member) or its defined fragments,
CC or which hybridises to it under stringent hybridisation conditions and
CC encodes a protein that exhibits Frazzled activity. Also included are a
CC vector comprising the above DNA molecule in operative association with an
CC expression control sequence, a host cell transformed with the vector, a
CC method for producing purified human SDF-5 protein, a purified human SDF-5
CC polypeptide, a composition comprising a therapeutic amount of at least
CC one human SDF-5 polypeptide cited above, a method for altering the
CC regulation of pancreatic genes in a patient (comprising administering to
CC the patient an amount of the composition cited above), antibodies to a
CC purified human SDF-5 protein and a method for increasing the
CC differentiation of cells into chondrocytes, comprising applying a
CC composition comprising BMP-2 (Bone morphogenetic protein-2) and SDF-5.
CC The DNA and protein are useful in regulating the binding of Wnt (wingnut)
CC genes to their receptor or in inducing formation, growth,
CC differentiation, proliferation and/or maintenance of chondrocytes and/or
CC cartilage tissue, and for other tissue repair, such as pancreatic tissue
CC repair. These may be used in the treatment of cartilage disorders, such
CC as osteoarthritis, rheumatoid arthritis or articular cartilage defects.
CC These may also be used for augmenting the activity of other tissue
CC regenerating and differentiation factors. In addition, the protein and
CC DNA are used as nutritional sources or supplements and in treating
CC various immune deficiencies and disorders (e.g. infections, HIV,
CC hepatitis, cancer, diabetes, inflammation or asthma) or neurological
CC disorders (e.g. Parkinson's disease, Alzheimer's disease or Huntington's
CC disease). The present sequence represents full length human SDF-5.
XX Sequence 295 AA;
SQ Query Match 100.0%; Score 1487; DB 7; Length 295;
Best Local Similarity 100.0%; Pred. No. 6, 4e-138;
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SARGLFLFGQPDFSKYRNCCKPFPANLQLCHGIEYQNNRPNLLGHETMKEVLEQAGAWI 60
DB 21 SARGLFLFGQPDFSKYRNCCKPFPANLQLCHGIEYQNNRPNLLGHETMKEVLEQAGAWI 80
QY 61 PLVMKQCHPDTKKFLCSLPAPVCLDDDETIQFCHSLCVQVKDRCAPVMSAFGFWPDM 120
DB 81 PLVMKQCHPDTKKFLCSLPAPVCLDDDETIQFCHSLCVQVKDRCAPVMSAFGFWPDM 140
QY 121 ECDRFPQNDLCIPLASSDHLPLATEAPKVCACKNKDDNDIMETLCRNDFAKIKV 180
DB 141 ECDRFPQNDLCIPLASSDHLPLATEAPKVCACKNKDDNDIMETLCRNDFAKIKV 200
QY 181 KEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWKDSLQCTCEBMDINAPYLV 240

Db 201 KEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWKDSLQCTCEBMDINAPYLV 260
QY 241 GQKGGELVITSVKRWQKGQREFKRISSIRKJQC 275
Db 261 GQKGGELVITSVKRWQKGQREFKRISSIRKJQC 295

RESULT 10
ADN40027
ID ADN40027 standard; protein; 295 AA.
XX AC ADN40027;
XX DT 17-JUN-2004 (first entry)
XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C397.
XX KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnerary; Gene therapy; vaccine.
XX OS Homo sapiens.
XX PN WO2003042661-A2.
XX PD 22-MAY-2003.
XX PF 13-NOV-2002; 2002WO-US036810.
XX PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397757P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX PA
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI: 2003-468649/44.
DR N-PSDB; ADN39810.
XX Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX Claim 12; SEQ ID NO C397; 1385pp; English.
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a

CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularisation syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a polypeptide of the invention.

XX
SQ Sequence 295 AA;

Query Match 100.0%; Score 1487; DB 7; Length 295;
Best Local Similarity 100.0%; Pred. No. 6.4e-138;

Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60
Db 21 SARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80

Qy 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKDRCAPVMSAFGFPWPDML 120
Db 81 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKDRCAPVMSAFGFPWPDML 140

Qy 121 ECDRFPQNDLCIPLASSDHLIPATEAPKVCEACKNKNDNDNDIMETLCKNDFALKIKV 180
Db 141 ECDRFPQNDLCIPLASSDHLIPATEAPKVCEACKNKNDNDNDIMETLCKNDFALKIKV 200

Qy 181 KEITYINRDTKILLETKSTIYKLVNGVSRDLKKSVLWKDSLOCTCEEMNDINAPYLVM 240
Db 201 KEITYINRDTKILLETKSTIYKLVNGVSRDLKKSVLWKDSLOCTCEEMNDINAPYLVM 260

Qy 241 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 275
Db 261 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 295

RESULT 11
ADN05090
ID ADN05090 standard; protein; 295 AA.

XX AC ADN05090;

XX DT 01-JUL-2004 (first entry)

XX DE Antipsoriatic protein sequence #724.

XX KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX OS Homo sapiens.

XX PN WO2004028479-A2.

XX PD 08-APR-2004.

XX PF 25-SEP-2003; 2003WO-US030907.

XX PR 25-SEP-2002; 2002US-0414006P.

XX PA (GETH) GENENTECH INC.

XX PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

XX PT Wu TD;

XX DR WPI; 2004-305105/28.

XX DR N-PSDB; ADN05089.

XX PT New PRO nucleic acid or polypeptide, useful for preparing a

XX PT pharmaceutical composition for diagnosing or treating psoriasis in a

XX PS mammal.

XX Claim 9; SEQ ID NO 1484; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.

XX SQ Sequence 295 AA;

Query Match 100.0%; Score 1487; DB 8; Length 295;
Best Local Similarity 100.0%; Pred. No. 6.4e-138;

Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 60
Db 21 SARGFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNMRLPNLLGHETMKEVLEQAGAWI 80

Qy 61 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKDRCAPVMSAFGFPWPDML 120
Db 81 PLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQPCHSVCVQVKDRCAPVMSAFGFPWPDML 140

Qy 121 ECDRFPQNDLCIPLASSDHLIPATEAPKVCEACKNKNDNDNDIMETLCKNDFALKIKV 180
Db 141 ECDRFPQNDLCIPLASSDHLIPATEAPKVCEACKNKNDNDNDIMETLCKNDFALKIKV 200

Qy 181 KEITYINRDTKILLETKSTIYKLVNGVSRDLKKSVLWKDSLOCTCEEMNDINAPYLVM 240
Db 201 KEITYINRDTKILLETKSTIYKLVNGVSRDLKKSVLWKDSLOCTCEEMNDINAPYLVM 260

Qy 241 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 275
Db 261 GQKGGELVITSVKRWQKGQREFKRSIRSKLQC 295

RESULT 12
ADR46694
ID ADR46694 standard; protein; 295 AA.

XX AC ADR46694;

XX DT 18-NOV-2004 (first entry)

XX DE Cancer-associated protein, SEQ ID 107.

XX KW Cytostatic; Gene Therapy; cancer; human.

XX OS Homo sapiens.

XX PN WO2004073657-A2.

XX PD 02-SEP-2004.

XX PF 19-FEB-2004; 2004WO-US005455.

XX PR 19-FEB-2003; 2003US-0448784P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Aziz N, Gish KC, Wilson KE, Zlotnik A;

XX DR WPI; 2004-652787/63.

XX DR N-PSDB; ADR46636.

XX PT Detecting a pathological cell in a patient for diagnosing or treating

XX PT cancer by detecting in a biological sample from the patient genes whose

XX PT expression are up-regulated or down-regulated in specific cancers.

XX PS Claim 1; SEQ ID NO 107; 375pp; English.

XX The present invention relates to a method for detecting cancer in a

XX CC patient. The method comprises detecting in a biological sample from the

XX CC patient a nucleotide or protein sequence comprising a sequence that is at

XX CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or

DR N-PSDB; AA234241.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders.
XX
PS
PS Claim 12; Fig 167; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as sources
CC of probes, primers, for chromosome mapping, and for generation of
CC antisense sequences. They can also be used to create transgenic animals.
CC The proteins can be used to treat a variety of diseases and disorders,
CC depending on their function. Diseases that may be treated include blood
CC coagulation disorders, cancers and cellular adhesion disorders. They may
CC also be used to raise antibodies. AA233891 to AA234338, and AA241685 to
CC AA241774 represent polynucleotide and polypeptide sequence given in the
CC exemplification of the present invention
XX
XX Sequence 295 AA;
SQ
Query Match 99.7%; Score 1483; DB 2; Length 295;
Best Local Similarity 99.6%; Pred. No. 1.6e-137;
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNNRLLPNLLGHETMKEVLEQAGAWI 60
Db 21 SARGFLFGQPDFSYKRSNCKPIPVNLQCHGIEYQNNRLLPNLLGHETMKEVLEQAGAWI 80
QY 61 PLVMKQCHPDTKFKFLCSLFAFVCLDDLETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 120
Db 81 PLVMKQCHPDTKFKFLCSLFAFVCLDDLETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 140
QY 121 ECDRFPQNDLCIPLASSDHLLPATEAPKVCACEAKNKNDDNDIMETLCKNDFALKIKV 180
Db 141 ECDRFPQNDLCIPLASSDHLLPATEAPKVCACEAKNKNDDNDIMETLCKNDFALKIKV 200
QY 181 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWKDSLOCTCEEMNDINAPYLVM 240
Db 201 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWKDSLOCTCEEMNDINAPYLVM 260
QY 241 GQKGGLVITSVKRWQKGQREFKRSIRKLCQ 275
Db 261 GQKGGLVITSVKRWQKGQREFKRSIRKLCQ 295
RESULT 14
ID AAB44304
XX AAB44304 standard; protein; 295 AA.
XX
AC AAB44304;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO697 (UNQ361) protein sequence SEQ ID NO:415.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
XX 18-FEB-2000; 2000WO-US004341.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.

PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0145698P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US028565.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX WPI; 2000-611443/58.
DR N-PSDB; AAC78560.
XX
XX Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
XX Claim 12; Fig 167; 636pp; English.
XX
PS AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytotstatic activity. The
CC of PRO polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells; e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
XX Sequence 295 AA;
SQ
Query Match 99.7%; Score 1483; DB 3; Length 295;
Best Local Similarity 99.6%; Pred. No. 1.6e-137;
Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNNRLLPNLLGHETMKEVLEQAGAWI 60
Db 21 SARGFLFGQPDFSYKRSNCKPIPVNLQCHGIEYQNNRLLPNLLGHETMKEVLEQAGAWI 80
QY 61 PLVMKQCHPDTKFKFLCSLFAFVCLDDLETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 120
Db 81 PLVMKQCHPDTKFKFLCSLFAFVCLDDLETIQCHSLCVQVKDRCAPVMSAFGFPWPDML 140
QY 121 ECDRFPQNDLCIPLASSDHLLPATEAPKVCACEAKNKNDDNDIMETLCKNDFALKIKV 180
Db 141 ECDRFPQNDLCIPLASSDHLLPATEAPKVCACEAKNKNDDNDIMETLCKNDFALKIKV 200
QY 181 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWKDSLOCTCEEMNDINAPYLVM 240
Db 201 KEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWKDSLOCTCEEMNDINAPYLVM 260
QY 241 GQKGGLVITSVKRWQKGQREFKRSIRKLCQ 275
Db 261 GQKGGLVITSVKRWQKGQREFKRSIRKLCQ 295
RESULT 15
ID ABB84861
XX ABB84861 standard; protein; 295 AA.
XX

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 10:17:03 ; Search time 26.3947 Seconds
(without alignments)
1075.364 Million cell updates/sec

Title: US-08-949-904A-2
Perfect score: 1594
Sequence: 1 MLQPGSLLLLFLASHCCLG.....MQKGQREPKRISIRKLCQ 295

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1594	100.0	295	2 JE0174	frizzled protein-2
2	616.5	38.7	317	2 JE0175	frizzled protein-1
3	279.5	17.5	537	2 JC7127	frizzled protein 4
4	272.5	17.1	568	2 T25162	Frizzled-1 protein
5	269	16.9	581	2 JC7086	FZD10 protein - hu
6	269	16.9	647	2 JE0337	Frizzled-1 protein
7	267.5	16.8	550	2 T37325	wingless protein r
8	264.5	16.6	574	2 JE0339	Frizzled-7 protein
9	262	16.4	565	2 JE0338	Frizzled-2 protein
10	259.5	16.3	641	2 A45054	probable intercell
11	241	15.1	694	2 S71786	wingless receptor
12	224.5	14.1	605	2 T31690	hypothetical prote
13	223	14.0	581	2 S03540	gene frizzled prot
14	220.5	13.8	1113	2 JE0315	low-density lipopr
15	216.5	13.6	666	2 JC7312	frizzled-3 protein
16	213.5	13.4	197	2 JC7735	frizzled-related p
17	205	12.9	706	2 JE0164	frizzled-6 protein
18	177.5	11.1	579	2 JC7629	membrane-type friz
19	152.5	9.6	1774	2 B56101	collagen alpha 1(X
20	133.5	8.4	526	2 T13484	frizzled protein h
21	119	7.5	581	2 B54665	netrin-2 precursor
22	100	6.3	793	2 JC5539	Smoothed protein
23	98.5	6.2	1342	2 A36223	kinase-related tra
24	95.5	6.0	1282	2 JE0120	glycoprotein A m
25	93.5	5.9	1339	2 JC4387	epidermal growth f
26	92.5	5.8	495	2 B70322	hypothetical prote
27	91	5.7	532	2 AE1964	Dnak-type molecula
28	91	5.7	1290	2 A55094	chromosomal protei
29	89.5	5.6	392	2 E81325	probable dihydroor

ALIGNMENTS

RESULT 1

JE0174
frizzled protein-2 - human
C:Species: Homo sapiens (man)
C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C:Accession: JE0174
R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.
Biochem. Biophys. Res. Commun. 247, 287-293, 1998
A:Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.
A:Reference number: JE0174; MUID:98308108; PMID:9642118
A:Accession: JE0174
A:Molecule type: mRNA
A:Residues: 1-295 <HUA>
A:Cross-references: UNIPROT:Q9HAP5
C:Genetics:
A:Map position: 4q

Query Match 100.0%; Score 1594; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 1e-118;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLQPGSLLLLFLASHCCLGSARGLF	FGQPDFSYKRSNCKP	PANLQCHGIEYQNRL	60
Db	1	MLQPGSLLLLFLASHCCLGSARGLF	FGQPDFSYKRSNCKP	PANLQCHGIEYQNRL	60
Qy	61	PNLLGHETMKVLEQAGAWIPLVMKQ	CHPDTKFLCSL	FAPVCLDDLD	120
Db	61	PNLLGHETMKVLEQAGAWIPLVMKQ	CHPDTKFLCSL	FAPVCLDDLD	120
Qy	121	VKRCAPVMSAFGFPWDMLECDR	PPQNDLCIPLASSDHL	LPAATEAPKCEACKNKND	180
Db	121	VKRCAPVMSAFGFPWDMLECDR	PPQNDLCIPLASSDHL	LPAATEAPKCEACKNKND	180
Qy	181	DDNDIMETLCKNDKFKLKVKEIYIN	RDTKIILETSKTIYK	LVGVSERDLKSVLWLK	240
Db	181	DDNDIMETLCKNDKFKLKVKEIYIN	RDTKIILETSKTIYK	LVGVSERDLKSVLWLK	240
Qy	241	DSLQCTCEEMNDINAPVLMQKQGG	ELVITSVKRWQKQRE	FKRISIRKLCQ	295
Db	241	DSLQCTCEEMNDINAPVLMQKQGG	ELVITSVKRWQKQRE	FKRISIRKLCQ	295

RESULT 2

JE0175
frizzled protein-1b - human
C:Species: Homo sapiens (man)
C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C:Accession: JE0175
R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.
Biochem. Biophys. Res. Commun. 247, 287-293, 1998
A:Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.
A:Reference number: JE0174; MUID:98308108; PMID:9642118

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A;Accession: JE0175
A:Molecule type: mRNA
A:Residues: 1-317 <HUA>
A;Cross-references: UNIPROT:O14780
C;Genetics:
A;Gene: hPRP-1b
A;Map position: 5q14.3-q12.1

Query Match      38.7%; Score 616.5; DB 2; Length 317;
Best Local Similarity 43.9%; Pred. No. 2.3e-41;
Matches 126; Conservative 50; Mismatches 94; Indels 17; Gaps 7;

QY 7 SLLLLFLASHCHCLGARGFLFLFG-QPDFSYKESNCKP-----IPANLQICHGIEYQNNRL 60
Db ALALLGALHWAHPARCEEYHYGWAQEPHGRSYSKPPQCLDIPADLPCHTGVGYRMR 73
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120
Db PNLLHESLAEVKQQAASSWLPALLAKRCHSDTQVFLCSLPAPVC---LDRPIYPCRSLCEA 130
QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPIASSDHLHPATEAP---KVCEACKN 177
Db 131 VRAGCAPLMEAYGFPWPEMLHCKFPDLNDLCIAVQFGH--LPAT--APPVTKICAQCEM 186
QY 178 KNDNDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVL 237
Db 187 EHSADG-LMEQCCSDFVVMRIKEIKTIENGDRKULIGAQKKKKLLKPGPLKRGKOTKRLVL 245
QY 238 WLKDSLQCTCEEMNDINAPLVMGQKGGELVITSVKRWQKQGRBFK 284
Db 246 HMKNGAGCCPQLDSLGSFLVWGRKVDGQLLLMAVYRWDKKNKEMK 292

RESULT 3
JC7127
frizzled protein 4 - human
C;Species: Homo sapiens (man)
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
A;Accession: JC7127
R;Kirikoshi, H.; Sagara, N.; Koike, J.; Tanaka, K.; Sekihara, H.; Hirai, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 264, 955-961, 1999
A;Title: Molecular cloning and characterization of human frizzled-4 on chromosome 11q14-
A;Reference number: JC7127; MUID:20012777; PMID:10544037
A;Accession: JC7127
A;Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-537 <KIR>
A;Cross-references: UNIPROT:Q9ULV1; GB:AB032417; DBJ:AB032417; NID:g6277265; PID:g62772
C;Genetics:
A;Gene: FZD4
A;Map position: 11 region q14 - q21
C;Superfamily: fruit fly frizzled protein

Query Match      17.5%; Score 279.5; DB 2; Length 537;
Best Local Similarity 31.4%; Pred. No. 1.9e-14;
Matches 69; Conservative 30; Mismatches 90; Indels 31; Gaps 8;

QY 4 GPGSLLLLFLASHCHCLGARGFLFLFGQPDFSYKRSNCKPPIPANLQICHGIEYQNNRLPNL 63
Db 16 GVGLSLGLLLQLLLLLGPARG---FGDEE---ERRCDPI--RISMVQNLGYNVTKMENL 66
QY 64 LGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQVKD 123
Db 67 VGHLEQTDAELQJTTFTPLIQYCCSQQLQFLCSYVPMCTEKNINIPGCGMCLSVKR 126
QY 124 RCAPVMSAFGFPWDMLECDRFPQND---LC-----IPLASSDHLHPATEAPKVC 172
Db 127 RCEPLVKFGFAPWPSLCSKFPQNDHNHMCMEGFGDEEVLPHKTIQGE-----C 181
QY 173 EACKNKNDNDIMETL-----CKNDPALKIK-VKEITYI 206
Db 182 HSVGNTSDQYIWKRSNLNVLKCGYDAGLYSRSAKEFTDI 221
```

RESULT 4

T25162

Frizzled-1 protein homolog - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T25162; T42210

R;Wild, A.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19989

A;Accession: T25162

A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A;Residues: 1-568 <WIL>

A;Cross-references: UNIPROT:O16147; EMBL:Z81128; PIDN:CAB03398.1; GSPDB:GN000019; CESP:T2

R;Rocheleau, C.E.; Downs, W.D.; Lin, R.; Wittmann, C.; Bei, Y.; Cha, Y.H.; Ali, M.; Pri

Cell 90, 707-716, 1997

A;Title: Wnt signaling and an APC related gene specify endoderm in early C. elegans embr

A;Reference number: Z15051; MUID:97433081; PMID:9288750

A;Accession: T42210

A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A;Residues: 1-568 <ROC>

A;Cross-references: EMBL:AF013953; NID:g2463673; PIDN:AAC47750.1; PID:g2463674

C;Genetics:

A;Gene: mom-5; T23D8.1

A;Map position: 1

A;Introns: 158/2; 280/1; 326/2; 407/1; 447/2; 520/2

C;Superfamily: fruit fly frizzled protein

Query Match 17.1%; Score 272.5; DB 2; Length 568;
Best Local Similarity 29.3%; Pred. No. 7.4e-14;
Matches 73; Conservative 38; Mismatches 97; Indels 41; Gaps 9;

QY 8 LLLFLASHCHCLGARGL---FLFGQPDFSYKRSNCKPPIPANLQICHGIEYQNNRLPNLL 64

Db 5 LLILFLFG--CLSDQRLSSTSISSMNGFSTR-KCEHI--TIPCKNLDYNTVFFNLL 59

QY 65 GHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQVKR 124

Db 60 GHTTQSEAGPAIAQFNPLIKVKCEDIRLFLCTVYAPVC-TVLEKPIQPCRELCLSAGK 118

QY 125 CAPVMSAFGFPWDMLECDRFPQDNDLCIPIASSDHLHPATEAPKVCCEACKNKNDND 184

Db 119 CESLMKKFGFQWPDQCNKFPV-TDLCVGNKSS-----SSNKKSSND 162

QY 185 IMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVLWKDSLQ 244

Db 163 V-----TFGVSTIANEVVLSPKKCPHHMTTSGSHFSLPLLSGRLPESL----- 207

QY 245 CTCEEMNDI 253

Db 208 -TCEADNQV 215

RESULT 5

JC7086

FZD10 protein - human

C;Species: Homo sapiens (man)

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: JC7086

R;Koike, J.; Takagi, A.; Miwa, T.; Hirai, M.; Terada, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 262, 39-43, 1999

A;Title: Molecular cloning of Frizzled-10, a novel member of the Frizzled gene family.

A;Reference number: JC7086; MUID:99382237; PMID:10448064

A;Accession: JC7086

A:Molecule type: mRNA

A;Residues: 1-581 <KOL>

A;Cross-references: UNIPROT:Q9ULW2; DBJ:AB027464; NID:g5834487; PIDN:BAA84093.1; PID:g5

A;Experimental source: fetal lung

C;Genetics:

A;Gene: Frizzled-10 (fzd-10)

C;Keywords: receptor; signal transduction; transmembrane protein

Query Match 16.8%; Score 267.5; DB 2; Length 550;
Best Local Similarity 33.3%; Pred. No. 1.8e-13;
Matches 59; Conservative 30; Mismatches 67; Indels 21; Gaps 5;

Qy 10 LLFLASHCCIGSARGILFLFGQPDFSYKRSNCKIPANLQLCHGIEYQNMLPNULLGHETM 69
:
Db 7 VLFL-----LLGSCALF-----GKRQRCEQT--TIPLCKGTGYNMTSPNSYGHEQ 52
: :

Qy 70 KEVLEQAGAWIPLVMKQCHPDTKKFCLSLFAPVCLDDLDDETIOPCHSLCVQVKDCRCPVM 129
:
Db 53 EEAGLEVHQHYPIVEVGCFQHLPFCITVTPTICQENYDKPIPLPCMELCWEARSKCSPIIM 112
: :

Qy 130 SAFGFPPWDMLECDRRFPQDNDLCIPLASSDHLLPATPEEAPKVCEA---CKNKDDDN 183
:
Db 113 AKYGRWPETLSCEALPKMSD----QMSTGNICAAAPPDTFKKHKGHHHKNQONQN 165
: :

RESULT 8
JE0339
Frizzled-7 protein - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C;Accession: JE0339
R;Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A;Title: Molecular cloning, differential expression, and chromosomal localization of hum
A;Reference number: JE0337; PMID:99032814; PMID:9813155
A;Accession: JE0339
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-574 <SAG>
A;Cross-references: UNIPROT:Q96B74; DDBJ:AB017365; NID:G3927886; PIDN:BAA34668.1; PID:G
C;Superfamily: fruit fly frizzled protein

Query Match 16.6%; Score 264.5; DB 2; Length 574;
Best Local Similarity 39.7%; Pred. No. 3.2e-13;
Matches 52; Conservative 23; Mismatches 47; Indels 9; Gaps 4;

Qy 31 PDFSYKRSNCKIPANLQLCHGIEYQNMLPNULLGHETMKVELEQAGAMTPLYMKQCHPD 90
:
Db 44 PDHGF----CQPI--SIPLCTDIAYNOTTLPNLLHTNOEDAGLEVHQFYPLVKVQCSP 97
: :

Qy 91 TKKFLCSLFAPVCLDDLDDETIOPCHSLCVQVKDCRCPVMSAFGPWMDLECDRRFPD-- 148
:
Db 98 LRFPLCSMAPVC-TVLDQAIPPCRLCERAGCGCALMNKFGQFWPERLRCENFVPVHA 156
: :

Qy 149 NLDCIPLASSD 159
: :

Db 157 GEICVGQNTSD 167
: :

RESULT 9
JE0338
Frizzled-2 protein - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C;Accession: JE0338
R;Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A;Title: Molecular cloning, differential expression, and chromosomal localization of hum
A;Reference number: JE0337; PMID:99032814; PMID:9813155
A;Accession: JE0338
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-565 <SAG>
A;Cross-references: UNIPROT:Q14332; DDBJ:AB017364; NID:G3927884; PIDN:BAA34667.1; PID:G
C;Superfamily: fruit fly frizzled protein

Query Match 16.4%; Score 262; DB 2; Length 565;
Best Local Similarity 35.2%; Pred. No. 5e-13;
Matches 56; Conservative 29; Mismatches 62; Indels 12; Gaps 5;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 10:54:34 ; Search time 114.895 Seconds
(without alignments)
1011.168 Million cell updates/sec

Title: US-08-949-904A-2

Perfect score: 1594

Sequence: 1 MLQPGSLLLFLASHCLIG.....WKGQREFKRISIRKLQC 295

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*

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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*

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19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*

20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*

21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1594	100.0	295	8	US-08-949-904-2
2	1594	100.0	295	14	US-10-177-293-142
3	1594	100.0	295	15	US-10-295-027-1345
4	1594	100.0	295	16	US-10-783-528-107
5	1594	100.0	295	17	US-10-847-972-78
6	1594	100.0	295	17	US-10-432-256-2
7	1590	99.7	295	9	US-09-978-293A-415
8	1590	99.7	295	9	US-09-978-697-415
9	1590	99.7	295	9	US-09-978-192A-415
10	1590	99.7	295	9	US-09-999-832A-415
11	1590	99.7	295	10	US-09-978-189-415

12	1590	99.7	295	10	US-09-978-608A-415
13	1590	99.7	295	10	US-09-978-585A-415
14	1590	99.7	295	10	US-09-978-191A-415
15	1590	99.7	295	10	US-09-978-403A-415
16	1590	99.7	295	10	US-09-978-564A-415
17	1590	99.7	295	10	US-09-999-833A-415
18	1590	99.7	295	10	US-09-981-915A-415
19	1590	99.7	295	10	US-09-978-824-415
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22	1590	99.7	295	10	US-09-978-423A-415
23	1590	99.7	295	10	US-09-978-193A-415
24	1590	99.7	295	10	US-09-999-830A-415
25	1590	99.7	295	10	US-09-978-757A-415
26	1590	99.7	295	10	US-09-978-187B-415
27	1590	99.7	295	10	US-09-978-643A-415
28	1590	99.7	295	10	US-09-978-375A-415
29	1590	99.7	295	10	US-09-978-298A-415
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31	1590	99.7	295	10	US-09-978-681A-415
32	1590	99.7	295	10	US-09-978-194A-415
33	1590	99.7	295	10	US-09-999-829A-415
34	1590	99.7	295	10	US-09-978-299A-415
35	1590	99.7	295	10	US-09-978-544A-415
36	1590	99.7	295	10	US-09-978-665A-415
37	1590	99.7	295	10	US-09-978-802A-415
38	1590	99.7	295	11	US-09-999-831A-415
39	1590	99.7	295	12	US-09-978-824-415
40	1590	99.7	295	14	US-10-017-081A-415
41	1590	99.7	295	14	US-10-167-749-415
42	1590	99.7	295	14	US-10-013-921A-415
43	1590	99.7	295	14	US-10-013-929A-415
44	1590	99.7	295	14	US-10-016-177A-415
45	1590	99.7	295	14	US-10-223-085-90

ALIGNMENTS

RESULT 1

US-08-949-904-2

Sequence 2, Application US/08949904

Publication No. US20030175855A1

GENERAL INFORMATION:

APPLICANT: Racie, Lisa

APPLICANT: Lavallie, Edward

TITLE OF INVENTION: HUMAN SDF-5 PROTEIN AND COMPOSITIONS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENETICS INSTITUTE, INC.

STREET: 87 CAMBRIDGE PARK DRIVE

CITY: CAMBRIDGE

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/949,904

FILING DATE: October 15, 1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: LAZAR, STEVEN R.

REGISTRATION NUMBER: 32,618

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8260

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 295 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-949-904-2

Query Match      100.0%; Score 1594; DB 8; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.9e-139;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
Db 1 MLQPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60

QY 61 PNLLGHETMKEVLEOAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTOPCHSLCVQ 120
Db 61 PNLLGHETMKEVLEOAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTOPCHSLCVQ 120

QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPLATEEAPKVCCEACKNKND 180
Db 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPLATEEAPKVCCEACKNKND 180

QY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLK 240
Db 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLK 240

QY 241 DSIQCTCEEMNDINAPYLVMGKQGGLVITSVKRWKQGQREFKRIISRIRKLOC 295
Db 241 DSIQCTCEEMNDINAPYLVMGKQGGLVITSVKRWKQGQREFKRIISRIRKLOC 295

RESULT 2
US-10-177-293-142
; Sequence 142, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 142
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-142

Query Match      100.0%; Score 1594; DB 14; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.9e-139;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
Db 1 MLQPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60

QY 61 PNLLGHETMKEVLEOAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTOPCHSLCVQ 120
Db 61 PNLLGHETMKEVLEOAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETTOPCHSLCVQ 120

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Db 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPLATEEAPKVCCEACKNKND 180

QY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLK 240
Db 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMWLK 240

QY 241 DSIQCTCEEMNDINAPYLVMGKQGGLVITSVKRWKQGQREFKRIISRIRKLOC 295
Db 241 DSIQCTCEEMNDINAPYLVMGKQGGLVITSVKRWKQGQREFKRIISRIRKLOC 295

RESULT 3
US-10-295-027-1345
; Sequence 1345, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynnne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1345
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1345

Query Match 100.0%; Score 1594; DB 15; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.9e-139;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOGPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
DB 1 MLOGPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
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DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120
QY 121 VKRCAPVMSAFGFPWPMLECDRFPQNDLCIPLASSDHLPLATEEAPKVCACKNKD 180
DB 121 VKRCAPVMSAFGFPWPMLECDRFPQNDLCIPLASSDHLPLATEEAPKVCACKNKD 180
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240
DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240
QY 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKQ 295
DB 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKQ 295

RESULT 4

US-10-783-528-107
; Sequence 107, Application US/10783528
; Publication No. US20040219579A1

; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt
; APPLICANT: Wileon, Keith
; APPLICANT: Zlorenik, Albert
; TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
; FILE REFERENCE: 05882.0191.NPUS01
; CURRENT APPLICATION NUMBER: US/10/783,528
; CURRENT FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-783-528-107

Query Match 100.0%; Score 1594; DB 16; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.9e-139;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOGPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
DB 1 MLOGPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
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DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120
QY 121 VKRCAPVMSAFGFPWPMLECDRFPQNDLCIPLASSDHLPLATEEAPKVCACKNKD 180
DB 121 VKRCAPVMSAFGFPWPMLECDRFPQNDLCIPLASSDHLPLATEEAPKVCACKNKD 180
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240
DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240

QY 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKQ 295
DB 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKQ 295

RESULT 5

US-10-847-972-78
; Sequence 78, Application US/10847972
; Publication No. US20050049195A1

; GENERAL INFORMATION:
; APPLICANT: ZOU YIMIN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION
; FILE REFERENCE: ARCD:395US
; CURRENT APPLICATION NUMBER: US/10/847,972
; CURRENT FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/470,913
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-847-972-78

Query Match 100.0%; Score 1594; DB 17; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.9e-139;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLOGPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120
QY 121 VKRCAPVMSAFGFPWPMLECDRFPQNDLCIPLASSDHLPLATEEAPKVCACKNKD 180
DB 121 VKRCAPVMSAFGFPWPMLECDRFPQNDLCIPLASSDHLPLATEEAPKVCACKNKD 180
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240
DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240
QY 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKQ 295
DB 241 DSLOQTCCEMNDINAPYLVMGKOGGELVITSVKRWQKGQREFKRSIRKQ 295

RESULT 6

US-10-432-256-2
; Sequence 2, Application US/10432256
; Publication No. US20050113291A1

; GENERAL INFORMATION:
; APPLICANT: Applied Research Systems ARS Holding N.V.
; TITLE OF INVENTION: Use of SARP-1 in the treatment and/or prevention of scleroderma
; FILE REFERENCE: EP 469 Y
; CURRENT APPLICATION NUMBER: US/10/432,256
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-432-256-2

Query Match 100.0%; Score 1594; DB 17; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.9e-139;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOGPGSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60

Db	1	MLQPGSLLLFLASHCCLGSARGLFLFGQPDFSKRSNCKPIPANLQCHGIEYQNNRL	60	PRIOR APPLICATION NUMBER: 60/077646
Qy	61	PNLLGHETMKVELEQAGAWIPLVMKQCHPDPTKKFLCSLFPVCLDDLDLDTIOPCHSLCVQ	120	PRIOR FILING DATE: 1998-03-11
Db	61	PNLLGHETMKVELEQAGAWIPLVMKQCHPDPTKKFLCSLFPVCLDDLDLDTIOPCHSLCVQ	120	PRIOR FILING DATE: 1998-03-12
Qy	121	VKQRCAPVMSAFGPPWMDLECDRFPQDNDLCIPLASSDHLPLPATEEAPKVCEACKNKND	180	PRIOR APPLICATION NUMBER: 60/078004
Db	121	VKQRCAPVMSAFGPPWMDLECDRFPQDNDLCIPLASSDHLPLPATEEAPKVCEACKNKND	180	PRIOR FILING DATE: 1998-03-13
Qy	181	DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDIKKSVLWLK	240	PRIOR APPLICATION NUMBER: 60/078886
Db	181	DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDIKKSVLWLK	240	PRIOR FILING DATE: 1998-03-20
Qy	241	DSLQCTCEEMNDINAPVLMVQKQGGLVITSVKRWQKGQREFKKISRSIRKLQOC	295	PRIOR APPLICATION NUMBER: 60/078936
Db	241	DSLQCTCEEMNDINAPVLMVQKQGGLVITSVKRWQKGQREFKKISRSIRKLQOC	295	PRIOR FILING DATE: 1998-03-25
RESULT 7				PRIOR APPLICATION NUMBER: 60/078910
US-09-978-295A-415				PRIOR FILING DATE: 1998-03-26
; Sequence 415, Application US/09978295A				PRIOR APPLICATION NUMBER: 60/079656
; Patent No. US20020156006A1				PRIOR FILING DATE: 1998-03-27
; GENERAL INFORMATION:				PRIOR APPLICATION NUMBER: 60/079689
; APPLICANT: Ashkenazi, Avi				PRIOR FILING DATE: 1998-03-27
; APPLICANT: Baker Kevin P.				PRIOR APPLICATION NUMBER: 60/079663
; APPLICANT: Botstein, David				PRIOR FILING DATE: 1998-03-27
; APPLICANT: Desnoyers, Luc				PRIOR APPLICATION NUMBER: 60/079786
; APPLICANT: Eaton, Dan				PRIOR FILING DATE: 1998-03-27
; APPLICANT: Ferrara, Napoleon				PRIOR APPLICATION NUMBER: 60/079920
; APPLICANT: Filvaroff, Ellen				PRIOR FILING DATE: 1998-03-30
; APPLICANT: Fong, Sherman				PRIOR APPLICATION NUMBER: 60/079923
; APPLICANT: Gao, Wei-Qiang				PRIOR FILING DATE: 1998-03-30
; APPLICANT: Gerber, Hanspeter				PRIOR APPLICATION NUMBER: 60/080105
; APPLICANT: Gerritsen, Mary E.				PRIOR FILING DATE: 1998-03-31
; APPLICANT: Goddard, Audrey				PRIOR APPLICATION NUMBER: 60/080165
; APPLICANT: Godowski, Paul J.				PRIOR FILING DATE: 1998-03-31
; APPLICANT: Grimaldi, J. Christopher				PRIOR APPLICATION NUMBER: 60/080194
; APPLICANT: Gurney, Austin L.				PRIOR FILING DATE: 1998-03-31
; APPLICANT: Hillan, Kenneth J.				PRIOR APPLICATION NUMBER: 60/080327
; APPLICANT: Kljavin, Ivar J.				PRIOR FILING DATE: 1998-04-01
; APPLICANT: Kuo, Sophia S.				PRIOR APPLICATION NUMBER: 60/080328
; APPLICANT: Napier, Mary A.				PRIOR FILING DATE: 1998-04-01
; APPLICANT: Pan, James;				PRIOR APPLICATION NUMBER: 60/080333
; APPLICANT: Paoni, Nicholas F.				PRIOR FILING DATE: 1998-04-01
; APPLICANT: Roy, Margaret Ann				PRIOR APPLICATION NUMBER: 60/080334
; APPLICANT: Shelton, David L.				PRIOR FILING DATE: 1998-04-01
; APPLICANT: Stewart, Timothy A.				PRIOR APPLICATION NUMBER: 60/081070
; APPLICANT: Tumas, Daniel				PRIOR FILING DATE: 1998-04-08
; APPLICANT: Williams, P. Mickey				PRIOR APPLICATION NUMBER: 60/081049
; APPLICANT: Wood, William I.				PRIOR FILING DATE: 1998-04-08
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic				PRIOR APPLICATION NUMBER: 60/081071
; FILE REFERENCE: P2630P1C11				PRIOR FILING DATE: 1998-04-08
; CURRENT APPLICATION NUMBER: US/09/978,295A				PRIOR APPLICATION NUMBER: 60/081195
; CURRENT FILING DATE: 2001-10-15				PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 09/918585				PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 2001-07-30				PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/062250				PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1997-10-17				PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/064249				PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1997-11-03				PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/065311				

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; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
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; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15

;
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
;
Query Match 99.7%; Score 1590; DB 9; Length 295;
Best Local Similarity 99.7%; Pred. No. 4.4e-139;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLQPGSLLLLFLASHCCCLSGARGLFLFGQPDFFSYKRSNCKPPIPANLQLCHGIEYQNMRL 60
Db 1 MLQPGSLLLLFLASHCCCLSGARGLFLFGQPDFFSYKRSNCKPPIPNLQLCHGIEYQNMRL 60
QY 61 PNLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCVQ 120
Db 61 PNLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQPCHSVCVQ 120
QY 121 VKDRCAPVMSARGFPPMDLECDREPQDNDLCIPLASSDHLFPATEEAPKVEACKNKND 180
Db 121 VKDRCAPVMSARGFPPMDLECDREPQDNDLCIPLASSDHLFPATEEAPKVEACKNKND 180
QY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240
Db 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240
QY 241 DSLQCTCEEMNDINAPYLVMGQKGGELVITSVKRWKQGBRFBFKRISRSIRKLQC 295
Db 241 DSLQCTCEEMNDINAPYLVMGQKGGELVITSVKRWKQGBRFBFKRISRSIRKLQC 295
;
RESULT 8
US-09-978-697-415
; Sequence 415, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC27
; CURRENT APPLICATION NUMBER: US/09/978,697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311

;	PRIOR APPLICATION NUMBER: 60/081819	
;	PRIOR FILING DATE: 1998-04-15	
;	PRIOR APPLICATION NUMBER: 60/081952	
;	PRIOR FILING DATE: 1998-04-15	
;	PRIOR APPLICATION NUMBER: 60/081838	
;	PRIOR FILING DATE: 1998-04-15	
;	PRIOR APPLICATION NUMBER: 60/082568	
;	PRIOR FILING DATE: 1998-04-21	
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;	PRIOR FILING DATE: 1998-04-21	
;	PRIOR APPLICATION NUMBER: 60/082704	
;	PRIOR FILING DATE: 1998-04-22	
;	PRIOR APPLICATION NUMBER: 60/082804	
;	PRIOR FILING DATE: 1998-04-22	
;	PRIOR APPLICATION NUMBER: 60/082700	
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;	PRIOR FILING DATE: 1998-04-22	
;	PRIOR APPLICATION NUMBER: 60/082796	
;	PRIOR FILING DATE: 1998-04-23	
;	PRIOR APPLICATION NUMBER: 60/083336	
;	PRIOR FILING DATE: 1998-04-27	
;	PRIOR APPLICATION NUMBER: 60/083322	
;	PRIOR FILING DATE: 1998-04-28	
;	PRIOR APPLICATION NUMBER: 60/083392	
;	PRIOR FILING DATE: 1998-04-29	
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;	PRIOR FILING DATE: 1998-04-29	
;	PRIOR APPLICATION NUMBER: 60/083558	
;	PRIOR FILING DATE: 1998-04-29	
;	PRIOR APPLICATION NUMBER: 60/083559	
;	PRIOR FILING DATE: 1998-04-29	
;	PRIOR APPLICATION NUMBER: 60/083500	
;	PRIOR FILING DATE: 1998-04-29	
;	PRIOR APPLICATION NUMBER: 60/083742	
;	PRIOR FILING DATE: 1998-04-30	
;	PRIOR APPLICATION NUMBER: 60/084366	
;	PRIOR FILING DATE: 1998-05-05	
;	PRIOR APPLICATION NUMBER: 60/084414	
;	PRIOR FILING DATE: 1998-05-06	
;	PRIOR APPLICATION NUMBER: 60/084441	
;	PRIOR FILING DATE: 1998-05-06	
;	PRIOR APPLICATION NUMBER: 60/084637	
;	PRIOR FILING DATE: 1998-05-07	
;	PRIOR APPLICATION NUMBER: 60/084639	
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;	PRIOR FILING DATE: 1998-05-07	
;	PRIOR APPLICATION NUMBER: 60/084643	
;	PRIOR FILING DATE: 1998-05-07	
;	PRIOR APPLICATION NUMBER: 60/084600	
;	PRIOR FILING DATE: 1998-05-07	
;	PRIOR APPLICATION NUMBER: 60/085338	
;	PRIOR FILING DATE: 1998-05-13	
;	PRIOR APPLICATION NUMBER: 60/085323	
;	PRIOR FILING DATE: 1998-05-13	
;	PRIOR APPLICATION NUMBER: 60/085582	
;	PRIOR FILING DATE: 1998-05-15	
;	PRIOR APPLICATION NUMBER: 60/085700	

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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match          99.7%; Score 1590; DB 9; Length 295;
Best Local Similarity 99.7%; Pred. No. 4.4e-139;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLQGGSLLLFLASHCCGSGARGLEFLGQPDFSYKRSNCKIPANLQICHGIEYQNMEL 60
Db 1 MLQGGSLLLFLASHCCGSGARGLEFLGQPDFSYKRSNCKIPVNLQICHGIEYQNMEL 60

QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIOPCHSLCQV 120
Db 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIOPCHSLCQV 120

QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPLATBEAPKVCEACKNKND 180
Db 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPLATBEAPKVCEACKNKND 180

QY 181 DNDIMETLCKNDFAIKVKIKETIYNRDTKILLETKSTIYKLVNGVSERDLKKSVMWLK 240
Db 181 DNDIMETLCKNDFAIKVKIKETIYNRDTKILLETKSTIYKLVNGVSERDLKKSVMWLK 240

QY 241 DLSQTCBMDNDINAPYLVNGKQGGELVITSVKRWKQSGREFKRSIRKLQC 295
Db 241 DLSQTCBMDNDINAPYLVNGKQGGELVITSVKRWKQSGREFKRSIRKLQC 295

RESULT 9
US-09-978-192A-415
; Sequence 415, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC9

; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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69	PRIOR FILING DATE: 1998-05-07	

[illegible]

APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.7%; Score 1590; DB 9; Length 295;

Best Local Similarity 99.7%; Pred. No. 4.4e-139;

Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MLOGPGLLLFLASHCCLGARGLFLGQDPDFSKRNCNKPANLQCHGIEYQNNRL 60
QY 61 PNLLGHETMKEVLEOAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQCHSLCVQ 120
DB 61 PNLLGHETMKEVLEOAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETIQCHSLCVQ 120
QY 121 VKRCAPVMSAFGFPWPMLECDREPDNDLCIPLASSDHLPLATEAPKVCACKKNND 180
DB 121 VKRCAPVMSAFGFPWPMLECDREPDNDLCIPLASSDHLPLATEAPKVCACKKNND 180
QY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240
DB 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVMWLK 240
QY 241 DLSQCTCEMNDINAPYLVMGKQGGELVITSVKRWQKGQREFKRISSIRKLQC 295
DB 241 DLSQCTCEMNDINAPYLVMGKQGGELVITSVKRWQKGQREFKRISSIRKLQC 295

RESULT 11

US-09-978-189-415

; Sequence 415, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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73	PRIOR FILING DATE:	1998-05-05

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38	PRIOR FILING DATE: 1998-05-15
39	PRIOR APPLICATION NUMBER: 60/085697

Query Match 99.7%; Score 1590; DB 10; Length 295;

Best Local Similarity 99.7%; Pred. No. 4.4e-139;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLQPGSLLLFLASHCCGASRGFLFGQDPDSFYKRSNCKPTANIQLCHGIEYQNRL	60
Db	1	MLQPGSLLLFLASHCCGASRGFLFGQDPDSFYKRSNCKPTPNVNLQCHGIEYQNRL	60
Qy	61	PNLLGHETMKVELEQAGAWIPLVMKQCHPDTKFLCSLPAPVCLDDLDDETIQPCSHLCVQ	120
Db	61	PNLLGHETMKVELEQAGAWIPLVMKQCHPDTKFLCSLPAPVCLDDLDDETIQPCSHLCVQ	120
Qy	121	VKDRCAPVMSAFGFPWPMLECDRFPQDNDLCTPLASSDHLLPATEAPKPVCEACKNND	180
Db	121	VKDRCAPVMSAFGFPWPMLECDRFPQDNDLCTPLASSDHLLPATEAPKPVCEACKNND	180
Qy	181	DDNDIMETLCKNDFALKI KVKETIYINRDKIILETKSKTIYKLVGYSERDLKKSVLWLK	240
Db	181	DDNDIMETLCKNDFALKI KVKETIYINRDKIILETKSKTIYKLVGYSERDLKKSVLWLK	240
Qy	241	DSLQCTCEBNNDINAPYLVMGQKGGEVLVTSVKRWQKGOREFKRSIRSKLQOC	295
Db	241	DSLQCTCEBNNDINAPYLVMGQKGGEVLVTSVKRWQKGOREFKRSIRSKLQOC	295

RESULT 12

US-09-978-608A-415'
; Sequence 415, Application US/09978608A
; Publication No. US2003004542A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Goddard, Audrey
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Daniel
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 415
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-415

Query Match 99.7%; Score 1590; DB 10; Length 295;
Best Local Similarity 99.7%; Pred. No. 4.4e-139;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MLOGPGSLLLLFLASHCHCLGSARGLFLFGQPDFSYKRSNCKPIPVNLQCHGIEYQNRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETIQPCHSCLVQ 120
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETIQPCHSCLVQ 120
QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLHPATEEAPKVCACKNKND 180
DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLHPATEEAPKVCACKNKND 180
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DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSERDLKKSVMWLK 240
QY 241 DLSQCTCEEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRISIRKLQOC 295
DB 241 DLSQCTCEEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRISIRKLQOC 295

RESULT 13
US-09-978-585A-415
; Sequence 415, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
```

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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 415
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-415

Query Match 99.7%; Score 1590; DB 10; Length 295;
Best Local Similarity 99.7%; Pred. No. 4.4e-139;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLOGPGSLLLLFLASHCHCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
DB 1 MLOGPGSLLLLFLASHCHCLGSARGLFLFGQPDFSYKRSNCKPIPVNLQCHGIEYQNRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETIQPCHSCLVQ 120
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETIQPCHSCLVQ 120
QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLHPATEEAPKVCACKNKND 180
DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLHPATEEAPKVCACKNKND 180
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSERDLKKSVMWLK 240
DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSERDLKKSVMWLK 240
QY 241 DLSQCTCEEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRISIRKLQOC 295
DB 241 DLSQCTCEEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRISIRKLQOC 295

RESULT 14
US-09-978-191A-415
; Sequence 415, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
```


APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match 99.7%; Score 1590; DB 10; Length 295;
Best Local Similarity 99.7%; Pred. No. 4.4e-139;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MLOQPGSLLLFLASHCCLSGARGFLFGQDPFSYKRSNCKRPIPNLQLCHGIEYQNMRL 60

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DB 61 PNLGLHETMKEVLEQAGAWIPLVMKQCHPDTKFKLCSLFAPVCLDDLDLDTIOPCHSLCVQ 120

QY 121 VKDRCAPVMSARFPWDMLECDRFPQNDLCIPLASSDHLPLATEAPKVCCEAKNKND 180
DB 121 VKDRCAPVMSARFPWDMLECDRFPQNDLCIPLASSDHLPLATEAPKVCCEAKNKND 180

QY 181 DNDIMETLCKNDPALKVKKEITYINRDTKILLETKSTIYKLVGVSERDLKKSVMWK 240
DB 181 DNDIMETLCKNDPALKVKKEITYINRDTKILLETKSTIYKLVGVSERDLKKSVMWK 240

QY 241 DLSLQCTCEEMNDINAPYLVMQKQGGLVITSVKRWQKQREFKRSIRKLQC 295
DB 241 DLSLQCTCEEMNDINAPYLVMQKQGGLVITSVKRWQKQREFKRSIRKLQC 295

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RESULT 15
US-09-978-403A-415
; Sequence 415, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728

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Db 241 ||||| DSLQCTCEMNDINAPYLVWGQKGGELVITSVKRWKQKQREFKRIKRSIRKLQC 295

Search completed: September 1, 2005, 11:13:50
Job time : 116.895 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2005, 10:25:34 ; Search time 31.5702 Seconds
(without alignments)
697.540 Million cell updates/sec

Title: US-08-949-904A-2
Perfect score: 1594
Sequence: 1 MLQSGSLLLFLASHCLLG.....WQKQREFKRISIRKLQC 295

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1586	99.5	296	4	US-09-148-545-237 Sequence 237, App
3	1557	97.7	295	4	US-08-937-067-2 Sequence 2, Appli
4	1140	71.5	212	4	US-08-937-067-4 Sequence 4, Appli
5	614.5	38.6	305	4	US-09-949-016-7706 Sequence 7706, Ap
6	614.5	38.6	317	4	US-08-937-067-6 Sequence 6, Appli
7	614.5	38.6	317	4	US-09-949-016-6300 Sequence 6300, Ap
8	606	38.0	313	4	US-09-546-043-3 Sequence 3, Appli
9	606	38.0	338	4	US-09-546-043-4 Sequence 4, Appli
10	604	37.9	313	4	US-09-514-885-1 Sequence 1, Appli
11	604	37.9	313	4	US-09-949-016-6299 Sequence 6299, Ap
12	602	37.8	314	4	US-08-937-067-7 Sequence 7, Appli
13	590	37.0	113	4	US-09-087-031E-24 Sequence 24, Appl
14	585	36.7	313	4	US-09-087-031E-4 Sequence 4, Appli
15	583.5	36.6	314	4	US-09-087-031E-3 Sequence 3, Appli
16	488	30.6	295	3	US-08-893-6548-6 Sequence 6, Appli
17	478	30.0	267	4	US-09-546-043-7 Sequence 7, Appli
18	459.5	28.8	246	4	US-09-546-043-6 Sequence 6, Appli
19	433.5	27.2	280	3	US-08-893-6548-4 Sequence 4, Appli
20	407	25.5	281	3	US-08-893-6548-2 Sequence 2, Appli
21	382	24.0	195	4	US-09-546-043-5 Sequence 5, Appli
22	353	22.1	109	4	US-09-087-031E-19 Sequence 19, Appl
23	275.5	17.3	572	4	US-08-937-067-13 Sequence 13, Appl
24	275	17.3	685	4	US-08-937-067-14 Sequence 14, Appl
25	270.5	17.0	585	4	US-08-937-067-9 Sequence 9, Appli
26	267.5	16.8	537	4	US-08-937-067-11 Sequence 11, Appl
27	263.5	16.5	323	3	US-08-878-474-7 Sequence 7, Appli

28	262	16.4	565	4	US-08-937-067-8 Sequence 8, Appli
29	260.5	16.3	114	4	US-09-087-031E-15 Sequence 15, Appli
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31	259.5	16.3	325	4	US-09-976-594-479 Sequence 479, App
32	259.5	16.3	371	4	US-09-949-016-7544 Sequence 7544, Ap
33	256.5	16.1	318	3	US-08-878-474-3 Sequence 3, Appli
34	251	15.7	55	4	US-09-621-976-3894 Sequence 20, Appl
35	244.5	15.3	114	4	US-09-087-031E-20 Sequence 20, Appl
36	241	15.1	115	4	US-09-087-031E-10 Sequence 10, Appli
37	238	14.9	229	4	US-09-546-043-8 Sequence 8, Appli
38	237	14.9	114	4	US-09-087-031E-21 Sequence 21, Appli
39	235	14.7	114	4	US-09-087-031E-12 Sequence 12, Appl
40	231	14.5	102	4	US-09-959-392-20 Sequence 20, Appl
41	229.5	14.4	112	4	US-09-087-031E-17 Sequence 17, Appli
42	228	14.3	111	4	US-09-087-031E-14 Sequence 14, Appli
43	227.5	14.3	1042	4	US-09-959-392-2 Sequence 2, Appli
44	227	14.2	111	4	US-09-087-031E-9 Sequence 9, Appli
45	222.5	14.0	666	4	US-08-937-067-10 Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-148-545-179
; Sequence 179, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 26 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23

1	EARLIER APPLICATION NUMBER: 60/047,584	1	EARLIER FILING DATE: 1997-08-22
2	EARLIER FILING DATE: 1997-05-23	2	EARLIER APPLICATION NUMBER: 60/056,880
3	EARLIER APPLICATION NUMBER: 60/047,500	3	EARLIER FILING DATE: 1997-08-22
4	EARLIER FILING DATE: 1997-05-23	4	EARLIER APPLICATION NUMBER: 60/056,894
5	EARLIER APPLICATION NUMBER: 60/047,587	5	EARLIER FILING DATE: 1997-08-22
6	EARLIER FILING DATE: 1997-05-23	6	EARLIER APPLICATION NUMBER: 60/056,911
7	EARLIER APPLICATION NUMBER: 60/047,492	7	EARLIER FILING DATE: 1997-08-22
8	EARLIER FILING DATE: 1997-05-23	8	EARLIER APPLICATION NUMBER: 60/056,636
9	EARLIER APPLICATION NUMBER: 60/047,598	9	EARLIER FILING DATE: 1997-08-22
10	EARLIER FILING DATE: 1997-05-23	10	EARLIER APPLICATION NUMBER: 60/056,874
11	EARLIER APPLICATION NUMBER: 60/047,613	11	EARLIER FILING DATE: 1997-08-22
12	EARLIER FILING DATE: 1997-05-23	12	EARLIER APPLICATION NUMBER: 60/056,910
13	EARLIER APPLICATION NUMBER: 60/047,582	13	EARLIER FILING DATE: 1997-08-22
14	EARLIER FILING DATE: 1997-05-23	14	EARLIER APPLICATION NUMBER: 60/056,864
15	EARLIER APPLICATION NUMBER: 60/047,596	15	EARLIER FILING DATE: 1997-08-22
16	EARLIER FILING DATE: 1997-05-23	16	EARLIER APPLICATION NUMBER: 60/056,631
17	EARLIER APPLICATION NUMBER: 60/047,612	17	EARLIER FILING DATE: 1997-08-22
18	EARLIER FILING DATE: 1997-05-23	18	EARLIER APPLICATION NUMBER: 60/056,845
19	EARLIER APPLICATION NUMBER: 60/047,632	19	EARLIER FILING DATE: 1997-08-22
20	EARLIER FILING DATE: 1997-05-23	20	EARLIER APPLICATION NUMBER: 60/056,892
21	EARLIER APPLICATION NUMBER: 60/047,601	21	EARLIER FILING DATE: 1997-08-22
22	EARLIER FILING DATE: 1997-05-23	22	EARLIER APPLICATION NUMBER: 60/047,595
23	EARLIER APPLICATION NUMBER: 60/043,580	23	EARLIER FILING DATE: 1997-05-23
24	EARLIER FILING DATE: 1997-04-11	24	EARLIER APPLICATION NUMBER: 60/057,761
25	EARLIER APPLICATION NUMBER: 60/043,568	25	EARLIER FILING DATE: 05-Sep-1997
26	EARLIER FILING DATE: 1997-04-11	26	EARLIER APPLICATION NUMBER: 60/047,599
27	EARLIER APPLICATION NUMBER: 60/043,314	27	EARLIER FILING DATE: 1997-05-23
28	EARLIER FILING DATE: 1997-04-11	28	EARLIER APPLICATION NUMBER: 60/047,588
29	EARLIER APPLICATION NUMBER: 60/043,569	29	EARLIER FILING DATE: 1997-05-23
30	EARLIER FILING DATE: 1997-04-11	30	EARLIER APPLICATION NUMBER: 60/047,585
31	EARLIER APPLICATION NUMBER: 60/043,311	31	EARLIER FILING DATE: 1997-05-23
32	EARLIER FILING DATE: 1997-04-11	32	EARLIER APPLICATION NUMBER: 60/047,586
33	EARLIER APPLICATION NUMBER: 60/043,671	33	EARLIER FILING DATE: 1997-05-23
34	EARLIER FILING DATE: 1997-04-11	34	EARLIER APPLICATION NUMBER: 60/047,590
35	EARLIER APPLICATION NUMBER: 60/043,674	35	EARLIER FILING DATE: 1997-05-23
36	EARLIER FILING DATE: 1997-04-11	36	EARLIER APPLICATION NUMBER: 60/047,594
37	EARLIER APPLICATION NUMBER: 60/043,669	37	EARLIER FILING DATE: 1997-05-23
38	EARLIER FILING DATE: 1997-04-11	38	EARLIER APPLICATION NUMBER: 60/047,589
39	EARLIER APPLICATION NUMBER: 60/043,312	39	EARLIER FILING DATE: 1997-05-23
40	EARLIER FILING DATE: 1997-04-11	40	EARLIER APPLICATION NUMBER: 60/047,593
41	EARLIER APPLICATION NUMBER: 60/043,313	41	EARLIER FILING DATE: 1997-05-23
42	EARLIER FILING DATE: 1997-04-11	42	EARLIER APPLICATION NUMBER: 60/047,614
43	EARLIER APPLICATION NUMBER: 60/043,672	43	EARLIER FILING DATE: 1997-05-23
44	EARLIER FILING DATE: 1997-04-11	44	EARLIER APPLICATION NUMBER: 60/043,578
45	EARLIER APPLICATION NUMBER: 60/043,315	45	EARLIER FILING DATE: 1997-04-11
46	EARLIER FILING DATE: 1997-04-11	46	EARLIER APPLICATION NUMBER: 60/043,576
47	EARLIER APPLICATION NUMBER: 60/048,974	47	EARLIER FILING DATE: 1997-04-11
48	EARLIER FILING DATE: 1997-06-06	48	EARLIER APPLICATION NUMBER: 60/047,501
49	EARLIER APPLICATION NUMBER: 60/056,886	49	EARLIER FILING DATE: 1997-05-23
50	EARLIER FILING DATE: 1997-08-22	50	EARLIER APPLICATION NUMBER: 60/043,670
51	EARLIER APPLICATION NUMBER: 60/056,877	51	EARLIER FILING DATE: 1997-04-11
52	EARLIER FILING DATE: 1997-08-22	52	EARLIER APPLICATION NUMBER: 60/056,632
53	EARLIER APPLICATION NUMBER: 60/056,889	53	EARLIER FILING DATE: 1997-08-22
54	EARLIER FILING DATE: 1997-08-22	54	EARLIER APPLICATION NUMBER: 60/056,664
55	EARLIER APPLICATION NUMBER: 60/056,893	55	EARLIER FILING DATE: 1997-08-22
56	EARLIER FILING DATE: 1997-08-22	56	EARLIER APPLICATION NUMBER: 60/056,876
57	EARLIER APPLICATION NUMBER: 60/056,630	57	EARLIER FILING DATE: 1997-08-22
58	EARLIER FILING DATE: 1997-08-22	58	EARLIER APPLICATION NUMBER: 60/056,881
59	EARLIER APPLICATION NUMBER: 60/056,878	59	EARLIER FILING DATE: 1997-08-22
60	EARLIER FILING DATE: 1997-08-22	60	EARLIER APPLICATION NUMBER: 60/056,909
61	EARLIER APPLICATION NUMBER: 60/056,662	61	EARLIER FILING DATE: 1997-08-22
62	EARLIER FILING DATE: 1997-08-22	62	EARLIER APPLICATION NUMBER: 60/056,875
63	EARLIER APPLICATION NUMBER: 60/056,872	63	EARLIER FILING DATE: 1997-08-22
64	EARLIER FILING DATE: 1997-08-22	64	EARLIER APPLICATION NUMBER: 60/056,862
65	EARLIER APPLICATION NUMBER: 60/056,882	65	EARLIER FILING DATE: 1997-08-22
66	EARLIER FILING DATE:		

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; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 295

Query Match          99.5%; Score 1586; DB 4; Length 295;
Best Local Similarity 99.3%; Pred. No. 7.8e-166;
Matches 293; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLOGPSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPANLQLCHGIEYQNMRL 60
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Db 1 MLOGPSLLLLFLASHCCCLGSARGLFLFGQPDFSYKRSNCKPIPVNQLCHGIEYQNMRL 60
   |||||

QY 61 PNLGLHETWKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFPVCLDLDLDTIOPCHSLCVQ 120
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Db 61 PNLGLHETWKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFPVCLDLDLDTIOPCHSLCVQ 120
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QY 121 VKDRCAPVMSAFGFPWPMLECDRFPQNDLCLPIASSDHLPLPATEEAPKVCEACKNKND 180
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Db 121 VKDRCAPVMSAFGFPWPMLECDRFPQNDLCLPIASSDHLPLPATEEAPKVCEACKNKND 180
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QY 181 DDNDIMETLCKNDFAIKVKKEITYINRDTKIILETKSTIYKJNGVSRDLKKSVMJLK 240
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Db 181 DDNDIMETLCKNDFAIKVKKEITYINRDTKIILETKSTIYKJNGVSRDLKKSVMJLK 240
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QY 241 DLSLOCTCEBMDINAPYLVMGQKGGLVITSVKRWQKGQRFKRSIRKLOC 295
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Db 241 DLSLOCTCEBMDINAPYLVMGQKGGLVITSVKRWQKGQRFKRSIRKLOC 295
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RESULT 2
US-09-148-545-237
; Sequence 237, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-09-04
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
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; EARLIER APPLICATION NUMBER: 60/040,334
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; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
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; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
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; EARLIER APPLICATION NUMBER: 60/043,580
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; EARLIER APPLICATION NUMBER: 60/043,311
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; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
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QY 58 MRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCFLPAPVCLDLDLDTIOPCHSL 117
DB 75 MYLPNLEHETMAEVKQQAASSVPLLNKNCHAGTQVFLCFLPAPVC---LDRPIYPCRWL 131
QY 118 CVQVKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPLATEAPKVCACKN 177
DB 132 CEAVRDSCEPVMOFGFYWPEMLKCDKFP-EGDVCIAMTPPNATEASKPQGGTTVCPPCDN 190
QY 178 KNDDNDIMETLCKNDFAIKIKVKEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVL 237
DB 191 ELKSE-AIIEHLCASEFALRMKIKVKEKNGDKIV--PKKKPLKLGPIKKDLKLV 247
QY 238 WLKDSLOQTCCEMNDINAPYLVMQKQGGELVITSVKRWKQKQREPKRISIRSLKQ 295
DB 248 YLKNAGADCPCHOLDNLSHHFLMGRKVKSYLLTAIHKWDKKNKBFQKFMKKNHEC 305

RESULT 9
US-09-546-043-4
; Sequence 4, Application US/09546043
; Patent No. 6600018
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffery et al.,
; TITLE OF INVENTION: SECRETED FRIZZLED RELATED PROTEIN, sFRP, FRAGMENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 53990
; CURRENT APPLICATION NUMBER: US/09/546,043
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-043-4

Query Match 38.0%; Score 606; DB 4; Length 338;
Best Local Similarity 41.6%; Pred. No. 5.9e-58;
Matches 124; Conservative 54; Mismatches 104; Indels 16; Gaps 6;
QY 6 GSLILLFLASHCCIGSARGFLFGQPD-----PSYKRSNCKIPANLQICHIEYQN 57
DB 16 GVLLALGASGRGLSEYDYSVF-QSDTGPYQSGRFYTKPPQCVDPADLRLCHNVGYK 74
QY 58 MRLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCFLPAPVCLDLDLDTIOPCHSL 117
DB 75 MYLPNLEHETMAEVKQQAASSVPLLNKNCHAGTQVFLCFLPAPVC---LDRPIYPCRWL 131
QY 118 CVQVKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPLATEAPKVCACKN 177
DB 132 CEAVRDSCEPVMOFGFYWPEMLKCDKFP-EGDVCIAMTPPNATEASKPQGGTTVCPPCDN 190
QY 178 KNDDNDIMETLCKNDFAIKIKVKEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVL 237
DB 191 ELKSE-AIIEHLCASEFALRMKIKVKEKNGDKIV--PKKKPLKLGPIKKDLKLV 247
QY 238 WLKDSLOQTCCEMNDINAPYLVMQKQGGELVITSVKRWKQKQREPKRISIRSLKQ 295
DB 248 YLKNAGADCPCHOLDNLSHHFLMGRKVKSYLLTAIHKWDKKNKBFQKFMKKNHEC 305

RESULT 10
US-09-514-885-1
; Sequence 1, Application US/09514885
; Patent No. 6656461
; GENERAL INFORMATION:
; APPLICANT: Imai, Kazuishi
; APPLICANT: D'Armiento, Jeanine
; TITLE OF INVENTION: NOVEL THERAPEUTIC TREATMENT OF CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 58483.app
; CURRENT APPLICATION NUMBER: US/09/514,885
; CURRENT FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Human
US-09-514-885-1

Query Match 37.9%; Score 604; DB 4; Length 313;
Best Local Similarity 39.8%; Pred. No. 8.7e-58;
Matches 121; Conservative 60; Mismatches 103; Indels 20; Gaps 6;
QY 3 QGPGSLLILLFLASHCCIGSAR-----GLFLGQDPDFSYKRSNCKIPANLQICH 51
DB 11 RGALGVLLALGAALLAVGSASEYDVVSFQSDTGPYQSGR--FYTKPPQCVDPADLRLCH 68
QY 52 GIEYQNMLPNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCFLPAPVCLDLDLDTI 111
DB 69 NVGYKMWLPNLLGHETMAEVKQQAASSVPLLNKNCHAGTQVFLCFLPAPVC---LDRPI 125
QY 112 QPCHSLCVQVKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLPLATEAPKV 171
DB 126 YPCRWLCEAVRDSCEPVMOFGFYWPEMLKCDKFP-EGDVCIAMTPPNATEASKPQGGTTV 184
QY 172 CEACKNKNDNDIMETLCKNDFAIKIKVKEITYINRDTKIILETKSKTIYKLVNGVSRD 231
DB 185 CPPCDNELKSE-AIIEHLCASEFALRMKIKVKEKNGDKIV--PKKKPLKLGPIKKD 241
QY 232 LKKSVMWLKDSLOQTCCEMNDINAPYLVMQKQGGELVITSVKRWKQKQREPKRISIR 291
DB 242 LKKLVLYLKNAGADCPCHOLDNLSHHFLMGRKVKSYLLTAIHKWDKKNKBFQKFMKKN 301
QY 292 KLQC 295
DB 302 NHEC 305

RESULT 11
US-09-949-016-6299
; Sequence 6299, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6299
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6299

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Matches 121; Conservative 60; Mismatches 103; Indels 20; Gaps 6;
QY 3 QGPGSLLILLFLASHCCIGSAR-----GLFLGQDPDFSYKRSNCKIPANLQICH 51
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DB 69 NVGYKMWLPNLLGHETMAEVKQQAASSVPLLNKNCHAGTQVFLCFLPAPVC---LDRPI 125

QY 112 QPCHSLCVOVKDCRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPLASSDHLLPATEAPKV 171
Db 126 YFCRWLCEAVRSCFVPMQFFGYWEMLKCDKFP-EGDVCIAMTPPNATEASKPGQGTIV 184
QY 172 CBAKRNKDDNDIMETLCKNDPALKIKVKEITYINRDTKIILETSKTIYKLVGVSERD 231
Db 185 CFPDNLKSE-AIIHLCASEFALRMKIKEVKENGDKKIV--PKKKPLKLGPIKKKDL 241
QY 232 LKXSVLWLDKSLQCTCEEMNDINAPYLVMOQGGELVITSVKRWKGOREFKRISRSIR 291
Db 242 LKXLVLKNGADCPCHQLDNLSHHFLIMGRKVKSYLLTAIHKWDKKNKEFKNFPMKMK 301
QY 292 KLOC 295
Db 302 NHEC 305
RESULT 12
US-08-937-067-7
; Sequence 7, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Umansky, Samuil
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSES: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-937-067-7
Query Match 37.8%; Score 602; DB 4; Length 314;
Best Local Similarity 40.1%; Pred. No. 1.5e-57;
Matches 120; Conservative 59; Mismatches 100; Indels 20; Gaps 6;
QY 8 LLLLFLASHCCLGASR-----GLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQ 56
Db 17 VLLALGAALLAVGASSEYDYVSFQSDIGFYQSGR--FVTKPPQCVDI PADRLRLCHNVGYK 74
QY 57 NWRLNLLGHETMKVLEQAGNWIPLVMKQCHPDTKKELCSLFAFPVCLDDLDDETQPCS 116
Db 75 KXVPLNLEHETMAEVKQAGSWVPLLNKNCHAGTQVFLCSLFAFVC---LDRPIYPCRW 131
QY 117 LCVQVKDCRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPLASSDHLLPATEAPKVCACK 176

Db 132 LCEAVRSCFVPMQFFGYWEMLKCDKFP-EGDVCIAMTPNPTEASKPGQGTIVCPD 190
QY 177 NKNDNDNDIMETLCKNDPALKIKVKEITYINRDTKIILETSKTIYKLVGVSERDLKXSV 236
Db 191 NELKSE-AIIHLCASEFALRMKIKEVKENGDKKIV--PKKKPLKLGPIKKKDLKLV 247
QY 237 LWLKDSLOCTCEEMNDINAPYLVMOQGGELVITSVKRWKGOREFKRISRSIRKLOC 295
Db 248 LYLKNGADCPCHQLDNLSHHFLIMGRKVKSYLLTAIHKWDKKNKEFKNFMKOMKNHCC 306
RESULT 13
US-09-087-031E-24
; Sequence 24, Application US/09087031E
; Patent No. 6479255
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
; FILE REFERENCE: 11613.13USII
; CURRENT APPLICATION NUMBER: US/09/087,031E
; CURRENT FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/087,031
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/050,417
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 24
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-087-031E-24
Query Match 37.0%; Score 590; DB 4; Length 113;
Best Local Similarity 92.9%; Pred. No. 6.5e-57;
Matches 105; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 40 CKPIPANLQCHGIEYQNMRLPNLLGHETMKVLEQAGNWIPLVMKQCHPDTKKFLCSLF 99
Db 1 CKPIPANLGLCHGIEYGNMRLPNLLGHETMKVLEGAGNWIPLVMKQCHPDTKKFLCSLF 60
QY 100 APVCLDDLDDETQPCCHSLCVOVKDCRCAPVMSAFGFPWPDMLCEDRFPQDNDLC 152
Db 61 APVCLDDLDDETQPCCHSLCVOVKDCRCAPVMSAFGFPWPDMLCEDRFPQDNDLC 113
RESULT 14
US-09-087-031E-4
; Sequence 4, Application US/09087031E
; Patent No. 6479255
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
; FILE REFERENCE: 11613.13USII
; CURRENT APPLICATION NUMBER: US/09/087,031E
; CURRENT FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/087,031
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/050,417
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-087-031E-4

Query Match 36.7%; Score 585; DB 4; Length 313;
Best Local Similarity 40.1%; Pred. No. 1.1e-55;
Matches 123; Conservative 53; Mismatches 105; Indels 26; Gaps 7;
QY 3 QQGSLLLLFLASHCCLGSA-----RGFLFGQDPDFSYKRSNCKPIPANLQCHGI 53
DB 11 RGALGVLLAALGAAVASEYDYVSGSDIGPYGSGRFTKPPGCVDPADLRLCHNV 70
QY 54 EYQNRNLPLNLLGHETMKEVLEAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDDLDDETQ 113
DB 71 GYKKWVLPNLLSHETMAEVKGASSWVPLLNKNCHAGTGVFLCSLFAFVC---LDRPIYP 127
QY 114 CHSLCVQKDRCAPVMSAFGFPWPMLECDRPPQNDLCIPLASSDHLPLPATEAPK--- 170
DB 128 CHWLCEAVRDSCEPVWGFYWPMLKCDKFP-EGDVCIAMTP-----PNATEASKPGG 181
QY 171 --VCBACNKNDDNDIMETLCKNDPALKIKVKEITYINRDTKIILETYSKTIYKLVGS 228
DB 182 TTVCPCCONELKSE-AIIHLCASEFALRMKIKVKKENGDKKIV--PKKKKPLKLGPIK 238
QY 229 ERDLKSVLWLKDSLQCTCEEEMNDINAPYLVMGQKGSELVITSVKRWKQKOREFKRISR 288
DB 239 KKDCLKVLVLYLKNAGADCPCHGLDNLSSHFLINGRKVKSGYLLTAHKWDKKNKEFKNFMK 298
QY 289 SIRKLOQ 295
DB 299 KKNKHEC 305

RESULT 15

US-09-087-031E-3
; Sequence 3, Application US/09087031E
; Patent No. 6479255
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
; FILE REFERENCE: 11613.13US11
; CURRENT APPLICATION NUMBER: US/09/087,031E
; CURRENT FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/087,031
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/050,417
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-087-031E-3

Query Match 36.6%; Score 583.5; DB 4; Length 314;
Best Local Similarity 42.5%; Pred. No. 1.6e-55;
Matches 116; Conservative 48; Mismatches 92; Indels 17; Gaps 6;
QY 28 FQQPDFSYKRSNCKPIPANLQCHGI EYQNRNLPLNLLGHETMKEVLEQAGAWIPLVMKQC 87
DB 46 YGSGRFTYKPPGCVDPADLRLCHNVGYKKWVLPNLLHETMAEVKGASSWVPLLNKNC 105
QY 88 HPDTKKFLCSLFAFVCLDDLDDETQFCHSLCVQKDRCAPVMSAFGFPWPMLECDRPPQ 147
DB 106 HAGTGVFLCSLFAFVC---LDRPIYPCRLCEAVRDSCEPVWGFYWPMLKCDKFP- 161
QY 148 DNDLCIPLASSDHLPLPATEAPK-----VCEACKNKNDDNDIMETLCKNDPALKIKVE 202
DB 162 EGDVCIAMTP-----PNATEASKPGGTTVCPCCONELKSE-AIIHLCASEFALRMKIKE 215
QY 203 ITYINRDTKIILETYSKTIYKLVGSERDLKSVLWLKDSLQCTCEEEMNDINAPYLVMGQ 262

DB 216 VKKENGDKKIV--PKKKKPLKLGPIKKKDLKKLVLYLKNAGADCPCHGLDNLSSHFLINGR 273
QY 263 KOGGELVITSVKRWKQKOREFKRISRSIRKLOQ 295
DB 274 KVKSGYLLTAHKWDKKNKEFKNFMKKNHEC 306
Search completed: September 1, 2005, 10:56:27
Job time : 32.5702 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2005, 09:41:17 ; Search time 120.588 Seconds
(without alignments)
946.152 Million cell updates/sec

Title: US-08-949-904A-2
Perfect score: 1594
Sequence: 1 MLQCGSLLLFLASHCLG.....WQKGQEFKRISIRKLCQ 295

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1594	100.0	295	2 AAW82588	AAW82588 Human ATG
2	1594	100.0	295	2 AAW49082	Aaw49082 Homo sapi
3	1594	100.0	295	2 AAY06923	Aay06923 Human sec
4	1594	100.0	295	5 ABG31499	ABg31499 Human sec
5	1594	100.0	295	6 ABUS5908	Abu55908 Human pro
6	1594	100.0	295	6 AAE34062	Aae34062 SARP 2 pr
7	1594	100.0	295	6 ABR47455	Abx47455 Breast ca
8	1594	100.0	295	7 ADF77693	Adf77693 Human ful
9	1594	100.0	295	7 ADN40027	Adn40027 Cancer/an
10	1594	100.0	295	8 ADN05090	Adn05090 Antipsori
11	1594	100.0	295	8 ADR46694	Adr46694 Cancer-as
12	1590	99.7	295	2 AAY411748	Aay411748 Human PRO
13	1590	99.7	295	3 AAB44304	Aab44304 Human PRO
14	1590	99.7	295	5 ABB84861	Abb84861 Human PRO
15	1590	99.7	295	5 ABB95467	Abb95467 Human ang
16	1590	99.7	295	6 ABO25250	Abos25250 Novel hum
17	1590	99.7	295	6 ABO72256	Abu72256 Novel hum
18	1590	99.7	295	6 ABU84936	Abu84936 Human sec
19	1590	99.7	295	6 ABU61134	Abu61134 Human PRO
20	1590	99.7	295	6 ABU80403	Abu80403 Human sec
21	1590	99.7	295	6 ADA24954	Ada24954 Novel hum
22	1590	99.7	295	6 ABO19705	Abol19705 Novel hum
23	1590	99.7	295	6 ADA12615	Ada12615 Human sec
24	1590	99.7	295	6 ABO19596	Abol19596 Novel hum
25	1590	99.7	295	7 ADB73921	Adb73921 Human PRO

ALIGNMENTS

RESULT 1
AAW82588
ID AAW82588 standard; propein; 295 AA.
XX AC AAW82588;
XX AC

DT 01-MAR-1999 (first entry)
DE Human ATG-1622 protein.

XX ATG-1622; SDF5; human; secreted ligand; 7-transmembrane receptor;
KW diagnosis; disease; screening; vaccine; inoculate; treatment; obesity;
KW heart disease; hypertension; kidney disease; insulin resistance;
KW lipodystrophy; diabetes; central nervous system; CNS; gene mapping;
KW linkage analysis.

XX Homo sapiens.

XX EP879887-A1.

XX PD 25-NOV-1998.

XX PF 14-MAY-1998; 98EP-00303809.

XX PR 21-MAY-1997; 97US-0047251P.

XX PR 13-JUN-1997; 97US-00874156.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX Hu E, Zhu Y;

XX WPI; 1998-596879/51.

XX N-PSDB; AAV69384.

XX New human secreted protein ATG-1622 polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of Central
PT Nervous System diseases and diabetes.

XX PS Claim 11; Page 22-23; 28pp; English.

XX This sequence represents the human ATG-1622 protein which is related to
CC murine secreted ligands for 7-transmembrane receptors and similar to
CC murine SDF5. ATG-1622 polypeptides and polynucleotides are useful for
CC diagnosing susceptibility to diseases by detecting mutations in the ATG-
CC 1622 gene and can diagnose diseases associated with ATG-1622 imbalance.
CC The polypeptides can be used to screen for agonists and antagonists which
CC can be used in treatment to activate or inhibit ATG-1622 activity. The
CC ATG-1622 polypeptide can be administered directly or as a vaccine to

CC inoculate against disease. Diseases which can be diagnosed, prevented or
 CC treated by the ATG-1622 polypeptide or polynucleotides include heart
 CC disease, hypertension, kidney diseases, obesity, insulin resistance,
 CC lipodystrophy, diabetes and central nervous system (CNS) diseases. The
 CC ATG-1622 polypeptide is also useful for mapping the gene to a chromosome,
 CC allowing gene inheritance to be studied through linkage analysis

XX Sequence 295 AA;

SQ Query Match 100.0%; Score 1594; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 4e-150;
 Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQPGSILLLLFLASHCCLGSGARGFLFGQPPFSYKRSNCKPIPANLQCHGIEYQNRL 60
 DB 1 MLQPGSLLLLFLASHCCLGSGARGFLFGQPPFSYKRSNCKPIPANLQCHGIEYQNRL 60
 QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKFKFLCSLFPVCLDDLETIQCHSLCVQ 120
 DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKFKFLCSLFPVCLDDLETIQCHSLCVQ 120
 QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLLPATEAPKVCEACKNKND 180
 DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLLPATEAPKVCEACKNKND 180
 QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSIVLWK 240
 DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSIVLWK 240
 QY 241 DSIQCTCEEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRSIRKLQC 295
 DB 241 DSIQCTCEEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRSIRKLQC 295

RESULT 2

AAW49082
 ID AAW49082 standard; protein; 295 AA.

XX AC AAW49082;

DT 09-NOV-1998 (first entry)

XX Homo sapiens SDF-5 protein.

XX SDF-5; frazzled; osteoarthritis; rheumatoid arthritis; cell formation;
 KW proliferation; differentiation; diabetes; pancreatic cancer;
 KW wound healing; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "signal peptide"

XX WO9835043-A1.

XX 13-AUG-1998.

XX 15-OCT-1997; 97WO-US018369.

XX 06-FEB-1997; 97US-00796153.

XX 08-MAY-1997; 97US-00848439.

XX (GEMV) GENETICS INST INC.

XX Lavallie ER, Racie LA;

XX WPI: 1998-447240/38.

XX N-PSDB; AAV32930.

XX Isolated DNA encoding human SDF-5 protein - useful for controlling
 PT growth, differentiation etc. of cells, particularly of chondrocytes for
 PT treatment of arthritis etc., also pancreatic cells.

XX PS Claim 18; Page 57-58; 69pp; English.

XX The sequence is that of human SDF-5, a member of the Frazzled protein
 CC family. Cells transfected with a vector containing the sequence are used
 CC to regulate genes, particularly pancreatic genes, or in combination with
 CC bone morphogenic protein 2 (BMP2), to increase differentiation of
 CC progenitor cells into chondrocytes. The protein may be used to treat
 CC osteoarthritis, rheumatoid arthritis, or articular cartilage defects,
 CC also to increase/inhibit cell formation, growth, differentiation,
 CC proliferation and/or maintenance in many other organs or tissues, e.g.
 CC for prevention or treatment of pancreatic cancer, diabetes (by inducing
 CC de novo formation of islet cells), other tissue defects, also to improve
 CC healing of wounds and to increase survival of nervous system cells, e.g.
 CC in cases of transplants. The coding sequence can be used in gene therapy,
 CC and its fragments to detect related mRNA, while the protein is also used
 CC to generate antibodies, useful for affinity purification and as
 CC immunoassay reagents. Many other potential uses/activities for the gene
 CC and its encoded are contemplated but not exemplified, e.g. as cytokines,
 CC immuno-suppressants or immunostimulants, regulators of haematopoiesis, as
 CC fertility-control agents, haemostatic or thrombolytic agents, anti-
 CC inflammatory agents, antimicrobials, modulators of biorhythms and many
 CC more

XX Sequence 295 AA;

QY Query Match 100.0%; Score 1594; DB 2; Length 295;
 DB Best Local Similarity 100.0%; Pred. No. 4e-150;
 Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQPGSILLLLFLASHCCLGSGARGFLFGQPPFSYKRSNCKPIPANLQCHGIEYQNRL 60

DB 1 MLQPGSLLLLFLASHCCLGSGARGFLFGQPPFSYKRSNCKPIPANLQCHGIEYQNRL 60

QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKFKFLCSLFPVCLDDLETIQCHSLCVQ 120

DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKFKFLCSLFPVCLDDLETIQCHSLCVQ 120

QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLLPATEAPKVCEACKNKND 180

DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLLPATEAPKVCEACKNKND 180

QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSIVLWK 240

DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSIVLWK 240

QY 241 DSIQCTCEEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRSIRKLQC 295

DB 241 DSIQCTCEEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRSIRKLQC 295

RESULT 3

AAW06923

ID AAW06923 standard; protein; 295 AA.

XX AC AAW06923;

XX 01-JUL-1999 (first entry)

XX Human secreted protein ligand ATG-1622 polypeptide.

XX Human; ATG-1622 polypeptide; secreted protein ligand; 7-TM receptor;
 KW frizzled family; heart disease; hypertension; kidney disease; obesity;
 KW insulin resistance; lipodystrophy; diabetes; CNS disease.

XX Homo sapiens.

XX CA2229436-A.

XX 21-NOV-1998.

XX 23-APR-1998; 98CA-02229436.

PR 21-MAY-1997; 97US-0047251P.
PR 13-JUN-1997; 97US-00874156.
PR 20-MAR-1998; 98US-00044885.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX Hu E, Zhu Y;
PI WPI; 1999-244679/21.
DR N-PSDB; AAX34662.
XX
XX New secreted protein ligand polypeptide (ATG-1622) of 7-TM (frizzled family) receptors, useful for diagnosis, prevention and treatment of obesity, lipodystrophy, hypertension and heart disease.
XX
XX Claim 11; Page 10-11; 42pp; English.
XX
XX This represents a human ATG-1622 polypeptide, a secreted protein ligand for 7-TM (frizzled family) receptors. ATG-1622 polypeptides and CC polynucleotides are useful for diagnosing a disease or susceptibility to a disease by determining the presence/absence of a mutation in the ATG-1622 gene, and/or analysing for the presence or amount of ATG-1622 expressed in the patient. ATG-1622 expressing cells are useful for CC identifying modulators of the polypeptide which are can be used to treat CC conditions associated with a lack or excess of ATG-1622 polypeptide. CC Diseases diagnosed, prevented or treated include heart disease, CC hypertension, kidney diseases, obesity, insulin resistance, CC lipodystrophy, diabetes and CNS diseases. ATG-1622 protein may be useful CC for treating or preventing the onset of obesity. ATG-1622 polypeptides CC are also useful for mapping genes to chromosomes, allowing gene CC inheritance to be studies through linkage analysis
XX
XX Sequence 295 AA;
SQ
Query Match 100.0%; Score 1594; DB 2; Length 295;
Best Local Similarity 100.0%; Pred. No. 4e-150;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MLQPGSLLLFLASHCCLGSLGARGFLFGQPPFSYKRSNCKIPANLQLCHGIEYQNRL 60
DB 1 MLQPGSLLLFLASHCCLGSLGARGFLFGQPPFSYKRSNCKIPANLQLCHGIEYQNRL 60
OY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTDKKFLCSLPAPVCLDLDLDTIQCHSLCQV 120
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTDKKFLCSLPAPVCLDLDLDTIQCHSLCQV 120
OY 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLPLPATEEAPKVCACKNKND 180
DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPLASSDHLPLPATEEAPKVCACKNKND 180
OY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMLK 240
DB 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKKSVMLK 240
OY 241 DLSLQCTCEBMNDINAPYLVWGKQGGELVITSVKRWKQGRFKRISIRKLQC 295
DB 241 DLSLQCTCEBMNDINAPYLVWGKQGGELVITSVKRWKQGRFKRISIRKLQC 295
RESULT 4
ABG31499
ID ABG31499 standard; protein; 295 AA.
XX
XX AC ABG31499;
XX
XX 09-SEP-2004 (revised)
DT 28-NOV-2002 (first entry)
XX
XX Human secreted apoptosis-related protein 1 (SARP-1).
XX
XX Human; secreted apoptosis-related protein 1; SARP-1; scleroderma; systemic sclerosis; fibrotic disease; liver cirrhosis; keloid; interstitial pulmonary fibrosis; Dupuytren's contracture; scarring;
KW

KW wound healing; postoperative adhesion; reactive fibrosis;
KW chronic heart failure; myocardial infarction; inflammatory disorder;
KW lung inflammation; idiopathic pulmonary fibrosis; systemic disease;
KW rheumatoid arthritis; anti-sclerotic; protein therapy.
XX
XX Homo sapiens.
OS Unidentified.
XX
XX Key Location/Qualifiers
FH Misc-difference 1..50
FT /note= "Theoretical N-terminal sequence of immature SARP-1"
FT
FT Cleavage-site 19..20
FT /note= "Position of 1st predicted signal cleavage"
FT Protein 21..295
FT /note= "Specifically claimed in Claim 2"
FT Protein 24..295
FT /note= "Specifically claimed in Claim 2"
FT Cleavage-site 24..25
FT /note= "Position of 2nd predicted signal cleavage"
FT Protein 25..295
FT /note= "Specifically claimed in Claim 2"
FT Protein 26..295
FT /note= "Specifically claimed in Claim 2"
FT Protein 27..295
FT /note= "Specifically claimed in Claim 2"
FT Protein 28..295
FT /note= "Specifically claimed in Claim 2"
FT Cleavage-site 36..37
FT /note= "Tryptic like cleavage"
FT Protein 37..295
FT /note= "Specifically claimed in Claim 2"
XX
XX WO200246225-A2.
XX
XX 13-JUN-2002.
XX
XX 30-NOV-2001; 2001WO-EP013992.
XX
XX 06-DEC-2000; 2000EP-00126771.
PR 17-AUG-2001; 2001EP-00118888.
XX
XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
XX Plater-Zyberk C, Power C, Colinge J;
XX
XX WPI; 2002-705807/76.
DR N-PSDB; ABS53585.
XX
XX Use of human Secreted Apoptosis-Related Protein (SARP)-1 and SARP-1 nucleic acids for the treatment of sclerosis, especially systemic sclerosis.
XX
XX Claim 2; Fig 5; 63pp; English.
XX
XX The present invention relates to the use of human secreted apoptosis-related protein 1 (SARP-1), SARP-1 nucleic acids and/or a substance which stimulates the release or potentiates the activity of endogenous SARP-1 for the treatment of scleroderma. The SARP-1 protein binds to and CC initiates signalling of the human SARP-1 receptor. The SARP-1 protein can CC be used in protein therapy, and the polynucleotide sequences encoding CC SARP-1 can be used in gene therapy. SARP-1 polypeptide and polynucleotide CC sequences, and pharmaceutical compositions comprising SARP-1 are useful CC for the treatment of scleroderma, especially systemic sclerosis. They may CC also be used to treat fibrotic diseases (e.g. liver cirrhosis, CC interstitial pulmonary fibrosis, Dupuytren's contracture, keloid and CC other scarring/wound healing abnormalities, postoperative adhesions and CC reactive fibrosis), chronic heart failure (particularly after myocardial CC infarction), disorders involving inflammation of the lung (e.g. CC idiopathic pulmonary fibrosis), and systemic diseases (e.g. rheumatoid CC arthritis). The present sequence represents human SARP-1
XX
XX Revised record issued on 09-SEP-2004 : Correction to Feature Table Key

```
XX SQ Sequence 295 AA;
Query Match 100.0%; Score 1594; DB 5; Length 295;
Best Local Similarity 100.0%; Pred. No. 4e-150;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOGPGLLLFLASHCCLGARGLFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNRL 60
DB 1 MLOGPGLLLFLASHCCLGARGLFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTDKKFLCSLPAPVCLDDLDDETQPCHSVCVQ 120
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTDKKFLCSLPAPVCLDDLDDETQPCHSVCVQ 120
QY 121 VKDRCAPVMSAFGFPWPDMLCDRFPQDNDLCIPLASSDHLPLATEAPKVCACKNKND 180
DB 121 VKDRCAPVMSAFGFPWPDMLCDRFPQDNDLCIPLASSDHLPLATEAPKVCACKNKND 180
QY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETSKTIYKLVGVSERDLKKSVMWLK 240
DB 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETSKTIYKLVGVSERDLKKSVMWLK 240
QY 241 DSIQCTCEEMNDINAPYLVWGQKGGLVITSVKRWKQGFREKFRISIRKLQ 295
DB 241 DSIQCTCEEMNDINAPYLVWGQKGGLVITSVKRWKQGFREKFRISIRKLQ 295

RESULT 5
ABU55908
ID ABU55908 standard; protein; 295 AA.
XX AC ABU55908;
XX DT 25-MAR-2003 (first entry)
XX DE Human protein SARP 2.
XX KW Notch; Wnt; embryonic stem cell; embryogenesis; human; differentiation;
KW ligand; Parkinson's disease; Huntington's disease; motor neuron disease;
KW heart disease; diabetes; liver disease; cirrhosis; renal disease; AIDS;
KW acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN WO200277204-A2.
XX PD 03-OCT-2002.
XX PF 25-MAR-2002; 2002WO-GB001195.
XX PR 23-MAR-2001; 2001GB-00007296.
XX PR 23-MAR-2001; 2001GB-00007299.
XX PR 17-APR-2001; 2001GB-00009346.
XX PA (AXOR-) AXORDIA LTD.
XX PI Andrews P, Walsh J, Gokhale P;
XX DR N-PSDB; ABX75335.
XX DR WPI; 2003-092852/08.
XX PT Modulating the differentiation of embryonic stem cells by providing
PT ligands which bind receptors in the Notch and Wnt pathways, useful for
PT treating diseases such as Parkinson's, Huntington's, heart disease,
PT diabetes and AIDS.
XX PS Disclosure; Fig 82; 121pp; English.
XX CC The invention relates to modulating the differentiation of an embryonic
CC stem cell, comprising: (a) providing a culture of embryonic stem cells;
CC (b) providing at least one ligand or its active binding fragment, capable
CC of binding its cognate receptor polypeptide expressed by the embryonic
```

```
CC stem cell; (c) forming a culture comprising embryonic stem cells and the
CC ligand; and (d) growing the cell culture. Also included are: (i)
CC Modulating the differentiation of embryonic stem cells, comprising: (a)
CC providing a cell transfected with a nucleic acid molecule selected from:
CC (i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic
CC acid molecule that hybridizes to the nucleic acid in (i), and which
CC encodes a ligand capable of modulating embryonic stem cell
CC differentiation, or capable of binding a Wnt receptor; or (iii) nucleic
CC acid molecules which are degenerate as a result of the genetic code to
CC the sequences of (i) or (ii); (b) forming a culture comprising the cell
CC identified in (a) with an embryonic stem cell; and (c) growing the
CC culture for the maintenance and/or differentiation of the embryonic stem
CC cell; (2) inhibiting the differentiation of embryonic stem cells,
CC comprising: (a) providing at least one polypeptide or its active
CC fragment, that are inhibitors of the Wnt signalling pathway; (b) forming
CC a culture comprising the cell identified in (a) with an embryonic stem
CC cell; and (c) growing the culture for the maintenance of embryonic stem
CC cells in an undifferentiated state; or (3) inhibiting the differentiation
CC of embryonic stem cells, comprising: (a) providing a cell transfected
CC with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt
CC inhibitory polypeptide; (ii) a molecule which hybridizes to the molecule
CC of (i) and encodes a polypeptide capable of inhibiting Wnt signalling;
CC and (iii) nucleic acid molecules which are degenerate as a result of the
CC genetic code to the sequences of (i) or (ii); (b) forming a culture
CC comprising the cell identified in (a) with an embryonic stem cell; and
CC (c) growing the culture for the maintenance of embryonic stem cells in an
CC undifferentiated state; and (4) A cell, therapeutic cell or cell culture
CC obtainable by any of the methods cited above. The therapeutic cell of the
CC present invention is useful in the treatment of an animal, preferably a
CC human, comprising administering a cell composition comprising embryonic
CC stem cells which have been induced to differentiate into at least one
CC cell-type. The cell is also useful for the manufacture of a composition
CC for use in treatment of diseases such as Parkinson's disease,
CC Huntington's disease, motor neuron disease, heart disease, diabetes,
CC liver disease (e.g. cirrhosis), renal disease and AIDS (acquired
CC immunodeficiency syndrome). The present sequence is represents a Wnt or
CC Notch pathway protein (i.e. a ligand for the method of the invention)
XX Sequence 295 AA;
SQ
```

```
Query Match 100.0%; Score 1594; DB 6; Length 295;
Best Local Similarity 100.0%; Pred. No. 4e-150;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLOGPGLLLFLASHCCLGARGLFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNRL 60
DB 1 MLOGPGLLLFLASHCCLGARGLFLFGQDPFSYKRSNCKPIPANLQCHGIEYQNRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTDKKFLCSLPAPVCLDDLDDETQPCHSVCVQ 120
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHDPTDKKFLCSLPAPVCLDDLDDETQPCHSVCVQ 120
QY 121 VKDRCAPVMSAFGFPWPDMLCDRFPQDNDLCIPLASSDHLPLATEAPKVCACKNKND 180
DB 121 VKDRCAPVMSAFGFPWPDMLCDRFPQDNDLCIPLASSDHLPLATEAPKVCACKNKND 180
QY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETSKTIYKLVGVSERDLKKSVMWLK 240
DB 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETSKTIYKLVGVSERDLKKSVMWLK 240
QY 241 DSIQCTCEEMNDINAPYLVWGQKGGLVITSVKRWKQGFREKFRISIRKLQ 295
DB 241 DSIQCTCEEMNDINAPYLVWGQKGGLVITSVKRWKQGFREKFRISIRKLQ 295

RESULT 6
AAE34062
ID AAE34062 standard; protein; 295 AA.
XX AC AAE34062;
XX DT 02-MAY-2003 (first entry)
XX
```

DE SARP 2 protein.
XX
KW Drug screening; toxicology assay; signalling pathway; SARP 2.
XX
OS Unidentified.
XX
PN WO200290992-A2.
XX
PD 14-NOV-2002.
XX
XX 29-APR-2002; 2002WO-GB001946.
XX
PR 04-MAY-2001; 2001GB-00011004.
XX
XX (AXOR-) AXORDIA LTD.
XX
XX Andrews P, Draper J, Walsh J;
PI
XX WPI; 2003-120579/11.
DR N-PSDB; AAD52560.
XX
XX Identifying biologically active agents comprises cloning transfected
PT cells into a cell array, exposing the array to an agent to be tested, and
PT detecting signals generated by a reporter molecule as a result of
PT exposure to the agent.
XX
XX Claim 16; Fig 76; 90pp; English.
XX
XX The present invention relates to a novel screening method which enables
XX the identification of biologically active agents which mediate their
XX effect through the activation of genes. The method involves providing a
XX population of cells stably transfected with a nucleic acid encoding a
XX reporter molecule, cloning the transfected cells into a cell array,
XX exposing the array to at least one agent to be tested and detecting a
XX signal generated by the reporter molecule as a result of exposure to the
XX agent. The method is useful in identifying biologically active agents and
XX the genes through which the agents act, in screening potential drugs for
XX their ability to activate certain drug targets in a high-throughput
XX assay, in identifying relationships between signalling pathways and
XX specific signals that could be useful in eventually directing the
XX differentiation of embryonic stem cells and in toxicology assays by
XX testing for unwanted activation or inhibition of specific signalling
XX pathways. The present sequence is SARP 2 protein used to illustrate the
XX method of the invention
XX
SQ Sequence 295 AA;

Query Match 100.0%; Score 1594; DB 6; Length 295;
Best Local Similarity 100.0%; Pred. No. 4e-150;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQGGSLLLFLASHCCCLGSGARGFLFGQDPFSYKRSNCKPPIANLQCHGIEYQNRL 60
Db 1 MLQGGSLLLFLASHCCCLGSGARGFLFGQDPFSYKRSNCKPPIANLQCHGIEYQNRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFPVCLDLDLDTIQCHSLCVQ 120
Db 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFPVCLDLDLDTIQCHSLCVQ 120
QY 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPIASSDHLHPATEAPKVEACKNKND 180
Db 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPIASSDHLHPATEAPKVEACKNKND 180
QY 181 DNDIMETLCKNDFAIKVKKITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWLK 240
Db 181 DNDIMETLCKNDFAIKVKKITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWLK 240
QY 241 DSIQCTCEEMNDINAPYLVMGQKQGGELVITSVKRWKQGRBFKRSIRKLQOC 295
Db 241 DSIQCTCEEMNDINAPYLVMGQKQGGELVITSVKRWKQGRBFKRSIRKLQOC 295

RESULT 7

ABR47455
ID ABR47455 standard; protein; 295 AA.
XX
AC ABR47455;
XX
DT 12-JUN-2003 (first entry)
XX
DE Breast cancer associated protein sequence SEQ ID NO:142.
XX
KW Human; breast cancer; cytostatic; gene therapy.
XX
XX Homo sapiens.
OS
XX WO2003004989-A2.
PN
XX 16-JAN-2003.
PD
XX 21-JUN-2002; 2002WO-US019669.
PF
XX 21-JUN-2001; 2001US-0299887P.
PR
XX 27-JUN-2001; 2001US-0301572P.
PR
XX 18-JUL-2001; 2001US-0306501P.
PR
XX 25-SEP-2001; 2001US-0325002P.
PR
XX 05-MAR-2002; 2002US-0362583P.
PR
XX 14-MAY-2002; 2002US-0380391P.
XX
XX (MILL-) MILLENIUM PHARM INC.
PA
XX
XX Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;
PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
PI Bast RC, Hortobagyi GN, Fuzsai L, Meric F, Sahin A, Mills GB;
XX
XX WPI; 2003-210381/20.
DR
XX N-PSDB; ACC50147.
XX
XX Breast cancer diagnosis or treatment by comparing the level of expression
PT of a marker in a patient sample with that in the control non-breast
PT cancer sample.
XX
XX Claim 1; SEQ ID NO 142; 128pp; English.
XX
XX The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and
CC ABR47386 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences from
CC the present invention have cytostatic activities and can be used in gene
CC therapy. The method is useful for diagnosing and treating breast cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 295 AA;

Query Match 100.0%; Score 1594; DB 6; Length 295;
Best Local Similarity 100.0%; Pred. No. 4e-150;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQGGSLLLFLASHCCCLGSGARGFLFGQDPFSYKRSNCKPPIANLQCHGIEYQNRL 60
Db 1 MLQGGSLLLFLASHCCCLGSGARGFLFGQDPFSYKRSNCKPPIANLQCHGIEYQNRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFPVCLDLDLDTIQCHSLCVQ 120
Db 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFPVCLDLDLDTIQCHSLCVQ 120
QY 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPIASSDHLHPATEAPKVEACKNKND 180
Db 121 VKDRCAPVMSAFGFPWPDMLCEDRFPQDNDLCIPIASSDHLHPATEAPKVEACKNKND 180

QY 181 DDNDIMETLCKNDFAALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSIVLWK 240
 Db |||||
 181 DDNDIMETLCKNDFAALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSIVLWK 240
 |||||
 QY 241 DSIQCTCEEMNDINAPYLVWGQKGGELVITSVKRWQKQREPKRISIRKLQC 295
 Db |||||
 241 DSIQCTCEEMNDINAPYLVWGQKGGELVITSVKRWQKQREPKRISIRKLQC 295
 |||||

RESULT 8

ADP77693
 ID ADF77693 standard; protein; 295 AA.

XX ADF77693;

XX 26-FEB-2004 (first entry)

XX Human full length Frazzled family protein SDF-5.

XX Human; Frazzled family protein; SDF-5; pancreatic gene;
 KW chondrocyte differentiation; cartilage tissue formation; tissue repair;
 KW pancreatic tissue repair; cartilage disorders; osteoarthritis;
 KW rheumatoid arthritis; articular cartilage defect; nutritional source;
 KW nutritional supplement; immune deficiency; infection; HIV infection;
 KW hepatitis; cancer; diabetes; inflammation; asthma; neurological disorder;
 KW Parkinson's disease; Alzheimer's disease; Huntington's disease.

XX Homo sapiens.

XX Location/Qualifiers

FT Key 1..20
 FT Peptide /note= "Signal peptide"
 FT Region 18..295
 FT /note= "Claimed in claim 2"
 FT Region 19..295
 FT /note= "Claimed in claim 2"
 FT Region 20..295
 FT /note= "Claimed in claim 2"
 FT Protein 21..295
 FT /label= Mature_SDF_5
 FT /note= "Claimed in claim 2"
 FT Region 22..295
 FT /note= "Claimed in claim 2"
 FT Region 23..295
 FT /note= "Claimed in claim 2"
 FT Region 24..295
 FT /note= "Claimed in claim 2"
 FT Region 25..295
 FT /note= "Claimed in claim 2"

XX US2003175855-A1.

PN 18-SEP-2003.

XX 15-OCT-1997; 97US-00949904.

XX 06-FEB-1997; 97US-00796153.

PR 08-MAY-1997; 97US-00848433.

XX (LAVA/) LAVALLIE E R.

PA (RACI/) RACIE L A.

XX Lavallie ER, Racie LA;

PI WPI; 2003-898533/82.

DR N-PSDB; ADF77692.

XX New human SDF-5 DNA, useful for inducing formation, growth,
 PT differentiation, proliferation or maintenance of chondrocytes or
 PT cartilage tissues, or as nutritional sources or supplements.

XX Claim 18; SEQ ID NO 2; 24pp; English.

CC The invention relates to an isolated DNA sequence encoding mature or full
 CC length human SDF-5 (a frazzled family member) or its defined fragments,
 CC or which hybridises to it under stringent hybridisation conditions and
 CC encodes a protein that exhibits Frazzled activity. Also included are a
 CC vector comprising the above DNA molecule in operative association with an
 CC expression control sequence, a host cell transformed with the vector, a
 CC method for producing purified human SDF-5 protein, a purified human SDF-5
 CC polypeptide, a composition comprising a therapeutic amount of at least
 CC one human SDF-5 polypeptide cited above, a method for altering the
 CC regulation of pancreatic genes in a patient (comprising administering to
 CC the patient an amount of the composition cited above), antibodies to a
 CC purified human SDF-5 protein and a method for increasing the
 CC differentiation of cells into chondrocytes, comprising applying a
 CC composition comprising BMP-2 (Bone morphogenetic protein-2) and SDF-5.
 CC The DNA and protein are useful in regulating the binding of Wnt (wingnut)
 CC genes to their receptor or in inducing formation, growth,
 CC differentiation, proliferation and/or maintenance of chondrocytes, such
 CC cartilage tissue, and for other tissue repair, such as pancreatic tissue
 CC repair. These may be used in the treatment of cartilage defects, such
 CC as osteoarthritis, rheumatoid arthritis or articular cartilage defects.
 CC These may also be used for augmenting the activity of other tissue
 CC regenerating and differentiation factors. In addition, the protein and
 CC DNA are used as nutritional sources or supplements and in treating
 CC various immune deficiencies and disorders (e.g. infections, HIV,
 CC hepatitis, cancer, diabetes, inflammation or asthma) or neurological
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease or Huntington's
 CC disease). The present sequence represents full length human SDF-5.

XX Sequence 295 AA;

Query Match 100.0%; Score 1594; DB 7; Length 295;

Best Local Similarity 100.0%; Pred. No. 4e-150; Indels 0; Gaps 0;
 Matches 295; Conservative 0; Mismatches 0;

QY 1 MLQPGSLLLLFLASHCCGSGARGLFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNRL 60

Db 1 MLQPGSLLLLFLASHCCGSGARGLFLFGQPDFSYKRSNCKPPIANLQCHGIEYQNRL 60

QY 61 PNLLGHETMKVLEQAGAWIPLVMKQCHPDPTKFLCSLFAFVCLDLDLDETTPCHSLCVQ 120

Db 61 PNLLGHETMKVLEQAGAWIPLVMKQCHPDPTKFLCSLFAFVCLDLDLDETTPCHSLCVQ 120

QY 121 VKRCAPVMSAFGPPWPDMLFCDFPQDNLCIPLASSDHLPLATEAPKVEACKNKND 180

Db 121 VKRCAPVMSAFGPPWPDMLFCDFPQDNLCIPLASSDHLPLATEAPKVEACKNKND 180

QY 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSIVLWK 240

Db 181 DDNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSIVLWK 240

QY 241 DSIQCTCEEMNDINAPYLVWGQKGGELVITSVKRWQKQREPKRISIRKLQC 295

Db 241 DSIQCTCEEMNDINAPYLVWGQKGGELVITSVKRWQKQREPKRISIRKLQC 295

RESULT 9

ADN40027

ID ADN40027 standard; protein; 295 AA.

XX ADN40027;

XX 17-JUN-2004 (first entry)

XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C397.

XX Human; differential expression; cancer; angiogenic disorder;
 KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
 KW inflammatory disease; autoimmune disease;
 KW retinal neovascularisation syndrome; scarring; uterine fibroid;
 KW detection; diagnosis; prognosis; drug screening; drug targeting;
 KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
 KW vulnery; gene therapy; vaccine.

QY 181 DDNDIMETLCKNDFAIKIVKKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240
DB 181 DDNDIMETLCKNDFAIKIVKKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240
QY 241 DSLQCTCEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRISIRKLOC 295
DB 241 DSLQCTCEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRISIRKLOC 295
RESULT 11
ADR46694
ID ADR46694 standard; protein; 295 AA.
XX
AC ADR46694;
XX
DT 18-NOV-2004 (first entry)
XX
DE Cancer-associated protein, SEQ ID 107.
XX
KW Cytostatic; Gene Therapy; cancer; human.
XX
OS Homo sapiens.
XX
PN WO2004073657-A2.
XX
XX
PD 02-SEP-2004.
XX
PF 19-FEB-2004; 2004WO-US005455.
XX
PR 19-FEB-2003; 2003US-0448784P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Aziz N, Gish KC, Wilson KE, Zlotnik A;
XX
DR WPI; 2004-652787/63.
DR N-PSDB; ADR46636.
XX
XX
PT Detecting a pathological cell in a patient for diagnosing or treating
PT cancer by detecting in a biological sample from the patient genes whose
PT expression are up-regulated or down-regulated in specific cancers.
XX
PS Claim 1; SEQ ID NO 107; 375pp; English.
XX
CC The present invention relates to a method for detecting cancer in a
CC patient. The method comprises detecting in a biological sample from the
CC patient a nucleotide or protein sequence comprising a sequence that is at
CC least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or
CC protein sequence (ADR46646-ADR46703). The method is useful for detecting
CC cancer for preparing a composition for diagnosing or treating cancer.
XX
SQ Sequence 295 AA;
Query Match 100.0%; Score 1594; DB 8; Length 295;
Best Local Similarity 100.0%; Pred. No. 4e-150;
Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQPGSLLLLFLASHCCIGSARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRL 60
DB 1 MLQPGSLLLLFLASHCCIGSARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETTPCHSLCVQ 120
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETTPCHSLCVQ 120
QY 121 VKDRCAPVMSAFGFPWDMLECDRPPQNDLICIPASSDHLPLPATEEAPKVCACKNKND 180
DB 121 VKDRCAPVMSAFGFPWDMLECDRPPQNDLICIPASSDHLPLPATEEAPKVCACKNKND 180
QY 181 DDNDIMETLCKNDFAIKIVKKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240
DB 181 DDNDIMETLCKNDFAIKIVKKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240

QY 241 DSLQCTCEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRISIRKLOC 295
DB 241 DSLQCTCEMNDINAPYLVMGQKGGLVITSVKRWQKGQREFKRISIRKLOC 295
RESULT 12
AA41748
ID AA41748 standard; protein; 295 AA.
XX
AC AA41748;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO697 protein sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
XX
PD 16-SEP-1999.
XX
PF 08-MAR-1999; 99WO-US005028.
XX
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079234P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080134P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.

PR	28-APR-1998;	98US-00833222P.	QY	1	MLQPGSLLLLFLASHCLASARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNNRL	60
PR	29-APR-1998;	98US-00833922P.	Db	1	MLQPGSLLLLFLASHCLASARGFLFGQPDFSYKRSNCKPIPVNLQCHGIEYQNNRL	60
PR	29-APR-1998;	98US-0083495P.				
PR	29-APR-1998;	98US-0083496P.				
PR	29-APR-1998;	98US-0083499P.	QY	61	PNLLGHETMKEVLRQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDDDDETIQPCHSVCVQ	120
PR	29-APR-1998;	98US-0083500P.	Db	61	PNLLGHETMKEVLRQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDDDDETIQPCHSVCVQ	120
PR	29-APR-1998;	98US-0083545P.				
PR	29-APR-1998;	98US-0083554P.				
PR	29-APR-1998;	98US-0083558P.	QY	121	VKRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKYCEACKNKND	180
PR	29-APR-1998;	98US-0083559P.	Db	121	VKRCAPVMSAFGFPWDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKYCEACKNKND	180
PR	30-APR-1998;	98US-0083742P.				
PR	05-MAY-1998;	98US-0084366P.	QY	181	DDNDIMETLCKNDPALKIKVKEITYINRDTKIIILETSKTIYKLVNGVSRDLKKSIVLWK	240
PR	06-MAY-1998;	98US-0084414P.	Db	181	DDNDIMETLCKNDPALKIKVKEITYINRDTKIIILETSKTIYKLVNGVSRDLKKSIVLWK	240
PR	06-MAY-1998;	98US-0084441P.				
PR	07-MAY-1998;	98US-0084598P.				
PR	07-MAY-1998;	98US-0084600P.	QY	241	DSLOCTCEEMNDINAPYLVMGQKQGGELVITSVKRWKGQREFKRISIRKLOC	295
PR	07-MAY-1998;	98US-0084637P.	Db	241	DSLOCTCEEMNDINAPYLVMGQKQGGELVITSVKRWKGQREFKRISIRKLOC	295
PR	07-MAY-1998;	98US-0084639P.				
PR	07-MAY-1998;	98US-0084640P.				
PR	07-MAY-1998;	98US-0084643P.				
PR	13-MAY-1998;	98US-0085338P.				
PR	13-MAY-1998;	98US-0085339P.				
PR	15-MAY-1998;	98US-0085573P.				
PR	15-MAY-1998;	98US-0085579P.				
PR	15-MAY-1998;	98US-0085580P.				
PR	15-MAY-1998;	98US-0085582P.				
PR	15-MAY-1998;	98US-0085689P.				
PR	15-MAY-1998;	98US-0085697P.				
PR	15-MAY-1998;	98US-0085700P.				
PR	15-MAY-1998;	98US-0085704P.				
PR	18-MAY-1998;	98US-0086023P.				
PR	22-MAY-1998;	98US-0086392P.				
PR	22-MAY-1998;	98US-0086414P.				
PR	22-MAY-1998;	98US-0086430P.				
PR	22-MAY-1998;	98US-0086486P.				
PR	28-MAY-1998;	98US-0087098P.				
PR	28-MAY-1998;	98US-0087106P.				
PR	28-MAY-1998;	98US-0087208P.				
PR	30-JUL-1998;	98US-0094651P.				
PR	11-SEP-1998;	98US-0100038P.				
FA	(GETH) GENENTECH INC.					
XX	Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;					
PI	WPI; 1999-551358/46.					
XX	N-PSDB; AAZ34241.					
DR	New secreted and transmembrane polypeptides and their polynucleotides,					
XX	useful for treating blood coagulation disorders, cancers and cellular					
PT	adhesion disorders.					
XX	Claim 12; Fig 167; 530pp; English.					
PS	The present invention describes secreted and transmembrane polypeptides					
XX	and their polynucleotides. The nucleotide sequences are useful as sources					
CC	of probes, primers, for chromosome mapping, and for generation of					
CC	antisense sequences. They can also be used to create transgenic animals.					
CC	The proteins can be used to treat a variety of diseases and disorders,					
CC	depending on their function. Diseases that may be treated include blood					
CC	coagulation disorders, cancers and cellular adhesion disorders. They may					
CC	also be used to raise antibodies. AA233891 to AA234339, and AA41685 to					
CC	AA41774 represent polynucleotide and polypeptide sequence given in the					
CC	exemplification of the present invention					
XX	Sequence 295 AA;					
QY	Query Match	99.7%; Score 1590; DB 2; Length 295;				
DR	Best Local Similarity	99.7%; Pred. No. ie-149;				
XX	Matches 294; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				

Novel PRO polypeptides and polynucleotides used in detection methods, to

PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.

XX Claim 12; Fig 167; 636pp; English.

XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytotactic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences

XX Sequence 295 AA;

Query Match 99.7%; Score 1590; DB 3; Length 295;
Best Local Similarity 99.7%; Pred. No. 1e-149;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLQPGSLLLLFLASHCCLGSARGLFLGQPDFSYKRSNCKPPIANLQCHGIEYQNMRL 60
DB 1 MLQPGSLLLLFLASHCCLGSARGLFLGQPDFSYKRSNCKPPIANLQCHGIEYQNMRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDLDLDTTPCHSLVCQ 120
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDLDLDTTPCHSLVCQ 120
QY 121 VKDRCAPVMSARGFPPWDMLECDRFPQNDLCPPLASSDHLPLATEAPKVCACKNKD 180
DB 121 VKDRCAPVMSARGFPPWDMLECDRFPQNDLCPPLASSDHLPLATEAPKVCACKNKD 180
QY 181 DNDIMETLCKNDFALKVKKEITYINRDTKILLETKSTIYKLVGVSERDLKKSVMWLK 240
DB 181 DNDIMETLCKNDFALKVKKEITYINRDTKILLETKSTIYKLVGVSERDLKKSVMWLK 240
QY 241 DLSQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKQREFKRSIRKLQC 295
DB 241 DLSQCTCEEMNDINAPYLVMGQKGGELVITSVKRWQKQREFKRSIRKLQC 295

RESULT 14
ABB84861
ID ABB84861 standard; protein; 295 AA.

XX AC ABB84861;

XX DT 16-MAY-2002 (first entry)

XX DE Human PRO697 protein sequence SEQ ID NO:90.

XX Human; angiogenesis; cardiast; cytotactic; antiangiogenic; hypotensive;
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.

XX OS Homo sapiens.

XX PN WO200200690-A2.

XX PD 03-JAN-2002.

XX PF 20-JUN-2001; 2001WO-US019692.

XX PR 23-JUN-2000; 2000US-0213637P.

XX PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 30-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 31-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.

(GETH) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-090516/12.

N-PSDB; ABL88116.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,
useful in diagnosis and treatment of cardiovascular (e.g. myocardial
infarction), endothelial or angiogenic disorders in a mammal.

Claim 11; Fig 90; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
angina, myocardial infarction, thrombophlebitis, lymphangitis, tumour
angiogenesis (such as breast carcinoma and liver carcinoma) and wound
healing. The PRO polynucleotides have applications in molecular biology,
including use as hybridisation probes, and in chromosome and gene
mapping. ABL88259 to ABL88267 represent primers and probes used in the
exemplification of the present invention

Sequence 295 AA;

Query Match 99.7%; Score 1590; DB 5; Length 295;
Best Local Similarity 99.7%; Pred. No. 1e-149;
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLQPGSLLLLFLASHCCLGSARGLFLGQPDFSYKRSNCKPPIANLQCHGIEYQNMRL 60
DB 1 MLQPGSLLLLFLASHCCLGSARGLFLGQPDFSYKRSNCKPPIANLQCHGIEYQNMRL 60

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QY	436	CCCAACCTGCTGGGCCACGAGACCATGAGGAGGTGCTGGAGCAGCCCGCGCTTGGATC	495
Db	61	ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluAlaGlyAlaTrpIle	80
QY	496	CGGCTGGTCATGAAGAGTGCACCCGGACACCAAGAAGTTCTGTGCTCGCTTCGCGC	555
Db	81	ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla	100
QY	556	CCGCTCGCTCGATGACCTACACGAGACCATCCAGCCATGCCACTCGCTCTCGCGTGAG	615
Db	101	ProValCysLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln	120
QY	616	GTGAAGGACCGCTGGCGCCCGCTCATGTCCGCGCTTCGGCTTCCTCGGCCCCACACATGTT	675
Db	121	ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu	140
QY	676	GAGTCGGACCGTTTCCCGCAGCAACGACCTTTGGATCCCGCTCGCTAGCAGCACAC	735
Db	141	GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis	160
QY	736	CTCCTGCCAGCCACCGAGGAGCTCCAAAGGTATGTGAGCCCTGCAAAATAAAAAATGAT	795
Db	161	LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp	180
QY	796	GATGACAAACGACATATGAAACGGCTTTGTAAAAATGATTTTGCATCGAAAAATAAAGTG	855
Db	181	AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal	200
QY	856	AAGGAGATAACTACATCAACCGAGATACCAAAATCATCTCGTGAGACCAAGACGACC	915
Db	201	LysGluIleThrTyrlleAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr	220
QY	916	ATTTACAAGCTGAACGGTGTGTCCAAAGGGACCTGAAGAAATCGGTGCTGGCTCAA	975
Db	221	IleThrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys	240
QY	976	GACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACGCGCCCTATCTGTGTCATG	1035
Db	241	AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProThrLeuValMet	260
QY	1036	GGACAGAAACAGGGTGGGAGCTGGTGATCATCTCGGTGAAGCGGTGGCAGAGGGGAG	1095
Db	261	GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln	280
QY	1096	AGAGAGTTCAAGCGCATCTCCCGCAGCATCCCGCAAGCTGCAGTGC	1140
Db	281	ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys	295
RESULT 2			
JF0175			
frezzed protein-lb - human			
C:Species: Homo sapiens (man)			
C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004			
C:Accession: JF0175			
R:Hu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D.			
Biochem. Biophys. Res. Commun. 247, 287-293, 1998			
A:Title: Tissue restricted expression of two human frzbs in preadipocytes and pancreas.			
A:Reference number: JF0174; MUID:98308108; PMID:9642118			
A:Accession: JF0175			
A:Molecule type: mRNA			
A:Residues: 1-317 <HUA>			
A:Cross-references: UNIPROT:O14780			
C:Genetics:			
A:Gene: hFRP-lb			
A:Map position: 5q14.3-q12.1			
Alignment Scores:			
Pred. No.:	5,356-33	Length:	317
Score:	618.00	Matches:	133
Percent Similarity:	60.00%	Conservative:	47
Best Local Similarity:	44.33%	Mismatches:	99
Query Match:	17.24%	Indels:	21

A:Reference number: JC7127; MUID:20012777; PMID:10544037

A:Accession: JC7127

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-537 <KIR>

A:Cross-references: UNIPROT:Q9ULV1; GB:AB032417; DBJ:AB032417; NID:g6277265; PID:g62772

C:Genetic:

A:Gene: F2D4

A:Map position: 11 region q14 - q21

C:Superfamily: fruit fly frizzled protein

Alignment Scores:
Pred. No.: 2,09e-11 Length: 537
Score: 290.00 Matches: 72
Percent Similarity: 45.26% Conservative: 33
Best Local Similarity: 31.03% Mismatches: 93
Query Match: 3.09% Indels: 34
DB: 2 Gaps: 9

US-08-949-904A-1 (1-2027) x JC7127 (1-537)

```
QY 238 CGGGTCGGCGCCGACGATGTCAGGGCCCTGGCTCGCTG-----CTGCTGCTC 288
Db 4 ArgGlyAlaGlyProSerValProGlyAlaProGlyGlyValGlyLeuSerLeuGlyLeu 23
QY 289 TTCTCTCGCTCGACTGCTGCTGGGCTCGCGCGGGCTCTTCTCTTTGGCCAGCCC 348
Db 24 LeuLeuGlnLeuLeuLeuGlyProAlaArgGly-----PheGlyAspGlu 40
QY 349 GACTTCTCTACAGCGCAGCAATTGCAAGCCCATCCCGCCCAACTCGAGCTGTGCCAC 408
Db 41 Glu-----GluArgCysAspProIle-----ArgIleSerMetCysGln 54
QY 409 GCATCGAATACAGAACATCGGCTGCCCACTGCTGGGCCACGAGACCATGAGGAG 468
Db 55 AsnLeuGlyTyrAsnValThrLysMetProAsnLeuValGlyHisGluLeuGlnThrAsp 74
QY 469 GTGCTGAGACGCGCGCTTGGATCCCGCTGGTTCATGAAGCAGTGCACCGGACACC 528
Db 75 AlaGluLeuGlnLeuThrPheThrProLeuIleGlnTyrGlyCysSerSerGlnLeu 94
QY 529 AAGAAGTCTCTGTGCTGCTTTCGCCCGCTGCTGCTGATGACCTAGACGAGACCATC 588
Db 95 GlnPhePheLeuCysSerValTyrValProMetCysThrGluLysIleAsnIleProIle 114
QY 589 CAGCCATGCCATCGCTCTGCTGCGAGGTGAAGACCGCTGGCCCGCTCATGTCGCGC 648
Db 115 GlyProCysGlyGlyMetCysLeuSerValLysArgCysGluProValLeuLysGlu 134
QY 649 TTCGGCTTCCCTGGCCGACATGCTTGAGTCGACCGTTTCCCGCAGGACCAACGAC--- 705
Db 135 PheGlyPheAlaTrpProGluSerLeuAenCysSerLysPheProProGlnAsnAspHis 154
QY 706 -----CTTTGC-----ATCCCTCTCGCTAGCAGCGACCAAC 735
Db 155 AsnHisMetCysMetGluGlyProGlyAspGluValProLeuProHisLysThrPro 174
QY 736 CTCCTGCGCAGCCAGGAGAGCTCCAAAGGTATGTGAAGCTGCAAAAATAAATGAT 795
Db 175 IleGlnProGlyGluGlu-----CysHisSerValGlyThrAsnSerAsp 189
QY 796 GATGACAACGACATAATGAAAGCTT-----TGTAATAATGATTGCA 840
Db 190 GlnTyrIleTrpValLysArgSerLeuAenCysValLeuLysCysGlyTyrAspAlaGly 209
QY 841 CTGAAAAATAAAA---GTGAAGGAGATAACCTACATC 873
Db 210 LeuTyrSerArgSerAlaLysGluPheThrAspIle 221
```

RESULT 4

JE0337

Frizzled-1 protein - human

C:Species: Homo sapiens (man)

C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

A:Accession: JE0337

R:Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.

Biochem. Biophys. Res. Commun. 252, 117-122, 1998

A:Title: Molecular cloning, differential expression, and chromosomal localization of human

A:Reference number: JE0337; MUID:99032814; PMID:9813155

A:Accession: JE0337

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-647 <SAG>

A:Cross-references: UNIPROT:Q9UP98; DBJ:AB017363; NID:g3927882; PIDN:BAA34666.1; PID:g93

C:Superfamily: fruit fly frizzled protein

Alignment Scores:
Pred. No.: 2,25e-11 Length: 647
Score: 289.50 Matches: 80
Percent Similarity: 43.87% Conservative: 31
Best Local Similarity: 31.62% Mismatches: 90
Query Match: 8.08% Indels: 52
DB: 2 Gaps: 10

US-08-949-904A-1 (1-2027) x JE0337 (1-647)

```
QY 45 GAGCCCCCGAGAGTGCAGGGGCTTGACGGCTTCGAGCGCTCCGCCGCTCTCCGGGTGCC 104
Db 33 GluGlySerGlyAspAlaGlyArgArgArgPro-----Pro 45
QY 105 GCTTCTCGCGCCCGCCAGCGCGG-----CTGCCA 134
Db 46 ValAspProArgArgLeuAlaArgGlnLeuLeuLeuLeuLeuTrpLeuGluAlaPro 65
QY 135 GCTTTTCGGGGCCCGAGTCGCACCCAGAGAGAGGGGGCGGGGCAAGCTCGAACT 194
Db 66 LeuLeuLeuGlyValArgAlaGlnAlaGlyGln---GlyProGlyGln----- 81
QY 195 CGCGCGCTCGCCTTCCCGGCTCCCTCTGCCCCCTCGGGGTGCGCGCCAC 254
Db 82 -----GlyProGlyProGlyGlnProPro-ProProGlnGlnGln 98
QY 255 GATGCTGAGGGCCCTGGCTGCTGCTCTCTCTCTCGCTCGACTGCTGCTGGG 314
Db 98 rGlyGlnGlnTyrAsnGlyGlu----- 105
QY 315 CTCGCGCGCGGGCTCTCTCTTTGGCCAGCGCCGACTTCTCTTACAGCGCAGCAATG 374
Db 106 -----ArgGlyIleSerVal-----ProAspHisGlyTyr-----Cy 116
QY 375 CAAGCCCATCCCGGCCAACCTGCACTGTGCCACGGCATCGAATACCAAGACATCGGCT 434
Db 116 sGlnProIle-----SerIleProLeuCysThrAspIleAlaTyrAsnGlnThrIle 134
QY 435 GCCCAACTGCTGGCGCCAGAGACCATGAAGAGAGTGTGGAGCAGGCGCGCTGGAT 494
Db 134 tProAsnLeuLeuGlyHisThrAsnGlnGluAspAlaGlyLeuGluValHisGlnPhe 154
QY 495 CCGCTGTGTCATGAAGCAGTGCACCCCGACACCAAGAGTTCTCTGTGCTCTCGC 554
Db 154 rProLeuValLysValGlnCysSerAlaGlnLeuLysPhePheLeuCysSerMetTyrAl 174
QY 555 CCGCTCTCGCTCGATGACCTAGACGAGACCATCCAGCCATGCCACTCGCTCTGGGTGA 614
Db 174 aProValCys---ThrValLeuGluGlnAlaLeuProCysArgSerLeuCysGluAr 193
QY 615 GGTGAAGACCGCTCGGCCCGGCTCATGTCCGCTTCCGCTTCCCTCGCGCCGACATGCT 674
Db 193 gAlaArgGlnGlyCysGluAlaLeuMetAsnLysPheGlyPheGlnTyrProAspThr 213
QY 675 TCAGTGCAGCCGTTTCCCGCAGGAC-----AACGACCTTTGCATCCCTCGCTAGCAG 728
Db 213 uLysCysGluLysPheProValHisGlyAlaGlyLeuLeuCysValGlyGlnAsnThr 233
QY 729 CGACCACCTCTCTCGCCAGCCCGAGGAAGCTCCAAAG 765
```

Db 233 rAspLysGlyThrProThrProSerLeuLeuProGlu 245
RESULT 5
A45054
probable intercellular signal transducer or transmitter Fz-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 02-Mar-2001
C:Accession: A45054
R:Chan, S.D.; Karpf, D.B.; Fowlkes, M.E.; Hooks, M.; Bradley, M.S.; Vuong, V.; Bambino, J. Biol. Chem. 267, 25202-25207, 1992
A:Title: Two homologs of the Drosophila polarity gene frizzled (fz) are widely expressed
A:Reference number: A45054; MUID:93094228; PMID:1334084
A:Accession: A45054
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-641 <CHA>
A:Experimental source: UMR 106 osteosarcoma cell line
A>Note: sequence extracted from NCBI backbone (NCBIP:120154)
C:Superfamily: fruit fly frizzled protein
Alignment Scores:
Pred. No.: 2,43e-11 Length: 641
Score: 289.00 Matches: 80
Percent Similarity: 46.28% Conservative: 32
Best Local Similarity: 33.06% Mismatches: 73
Query Match: 8.06% Indels: 57
DB: 2 Gaps: 12
US-08-949-904A-1 (1-2027) x A45054 (1-641)
QY 81 CGCCGCGCTCC--TCCGCGGTCCGCTTCTCCGGGCCCGAGCGCGGCTG----- 131
Db 42 ArgProArgAlaHisSerArgCysTrpAla-----ArgGlyLeuLeuLeu 56
QY 132 -----CCAGCTTTTCGGGGCCCGAGTCGCACCCAGCGAAGAGA 170
Db 57 LeuLeuTrpLeuLeuGluAlaProLeuLeuLeuGlyValArgAlaGlnProAlaGlyGln 76
QY 171 -----GGGGGCGGGCAAGCTCGAAGCTCGGGCGGCTGCCCTCCCGGCTCCGCTCC 227
Db 77 ValSerGlyProGlyGlnArgProPro-ArgProGlnProGln----- 91
QY 228 TCTGCCCCCTCGGGTCGGCGCCCGACGATGTCGAGGCGCCTGCTCGCTGCTGCT 287
Db 92 -----GlnGlyGlyGlnGln----- 96
QY 288 CTTCCTCGCTCGCACTGCTGCTGCGGCTCGGCGCGGGCTCTTCTCTTTGGCGAGCC 347
Db 97 -----TyrAsnGlyGluArgGlyIleSerIle-----Pr 106
QY 348 CGACTTCTCTACAAGCGAGCAATTGCAGCCGATCCGGGCCAACCTGCGAGCTGTGCCA 407
Db 106 oAspHisGlyTyr-----CysGlnProIle-----SerIleProLeuCysTh 120
QY 408 CGCGCTCGAATACCAGAACATCGCGCTGCCCACTGCTGGGCCACGAGACCATCAAGGA 467
Db 120 rAspIleAlaIleAsnGlnThrIleMetProAsnLeuLeuGlyHisThrAsnGlnGluAs 140
QY 468 GGTGTGGAGAGCGCGGCTTGGATCCCGTGTGCATGAAGCAGTGCACCCCGGACAC 527
Db 140 pAlaGlyLeuGluValHisGlnPheTyrProLeuValLysValGlnCysSerAlaGluLe 160
QY 528 CAGAAGTTCCTGCTGCTCTTCCGCCCCGCTGCTGCTGATGACCTAGACGAGACCAT 587
Db 160 ulysPheLeuCysSerMetTyrAlaProValCys---ThrValLeuGluGlnAlaLe 179
QY 588 CCAGCCATGCCACTCGCTCGGTGCAGGTGAAGACCGCTGCGCCCCGGTCACTCGCG 647
Db 179 uProProCysArgSerLeuCysGluArgAlaGlnGly---CysGluAlaLeuMetAsnLys 198
QY 648 CTTCGGCTTCCCTCGCCGACATCTTGAAGTCGACCGCTTTCCCGCAGGAC-----AA 701
Db 198 ePheGlyPheGlnTrpProAspThrLeuLysCysGluLysPheProValHisGlyArgG1 218

QY 702 CGACCTTTGCATCCCCCTCGCTAGCAGCGACCACTCTCTGCAGCCACCGAGAGCTCC 761
Db 218 yGluLeuCysValGlyGlnAsnThrSerAspLysGlyThrProThrProSerLeuLeuPr 238
QY 762 AAAG 765
Db 238 oGlu 239
RESULT 6
T25162
Frizzled-1 protein homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25162; T42210
R:Wild, A.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19989
A:Accession: T25162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-568 <WIL>
A:Cross-references: UNIPROT:O16147; EMBL:Z81128; PIDN:CA803398.1; GSPDB:GN00019; CESP:T2
A:Experimental source: clone T23D8
R:Rocheleau, C.E.; Downs, W.D.; Lin, R.; Wittmann, C.; Bei, Y.; Cha, Y.H.; Ali, M.; Prie
Cell 90, 707-716, 1997
A:Title: Wnt signaling and an APC related gene specify endoderm in early C. elegans embr
A:Reference number: Z15051; MUID:97433081; PMID:9288750
A:Accession: T42210
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-568 <ROC>
A:Cross-references: EMBL:AF013953; NID:G2463673; PIDN:AAC47750.1; PID:G2463674
C:Genetics:
A:Map position: 1
A:Introns: 158/2; 280/1; 326/2; 407/1; 447/2; 520/2
C:Superfamily: fruit fly frizzled protein

Alignment Scores:
Pred. No.: 2,96e-10 Length: 568
Score: 272.50 Matches: 73
Percent Similarity: 44.58% Conservative: 38
Best Local Similarity: 29.32% Mismatches: 97
Query Match: 7.60% Indels: 41
DB: 2 Gaps: 9

US-08-949-904A-1 (1-2027) x T25162 (1-568)

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QY 331 ---TTCCTCTTTGGCCAGCGCGAGCTTCTCTTACAGCGCGAGCAATTGCAAGCCATCCCG 387
Db 23 ThrSerIleSerSerMetAsnGlyPheSerThrThrArg---LysCysGluHisIle--- 40
QY 388 GCCAACCTGCGAGTGTGCCAGCGCATCAATACAGAACATGCGGCTGCCCACTGCTG 447
Db 41 ---ThrIleProMetCysLysAsnLeuAspTyrAsnGlnThrValPheProAsnLeuLeu 59
QY 448 GGCCACGAGACCATGAAGGAGGTGCTGGAGCAGCGCGGCTTGGATCCCGCTGTCATG 507
Db 60 GlyHisThrGlnSerGluAlaGlyProAlaIleAlaGlnPheAsnProLeuIleLys 79
QY 508 AAGCAGTGCACCCCGGACACCAAGATTCCTGTGCTGCTCTTCGCCCGCCGCTGTCGCTC 567
Db 80 ValLysCysSerGluAspIleArgLeuPheLeuCysThrValTyrAlaProValCys--- 98
QY 568 GATGACTTAGACGAGACCATCCAGCCATGCCACCTCGCTCTCGCTGAGTGAAGAGCGC 627
Db 99 ThrValLeuGluLysProIleGlnProCysArgGluLeuCysLeuSerAlaLysAsnGly 118


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Qy 574 CTAGCAGAGACCATTCAAGCATCGCACTCGCTCTGCGTGCAGGTGAAGACCGCTGCGCC 633
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Qy 634 CCGGTCATGTCGGCTTCGCCCTCGCCCGACATGCTTCAGTGCAGCGTTTCGCC 693
Db 136 LysLeuMetLysThrTyrAspHeAsnTrpProGluAsnLeuGluCysSerLysPhePro 155
Qy 694 -----CAGGACACAGCATCTTGCAATCCCGCTCGCTAGC 726
Db 156 ValHisGlyGlyAspLeuCysValAlaGluAsn-ThrThrSerSerAlaSerThrAl 175
Qy 727 AGCGACC-----ACCTCTGCCA 744
Db 175 aAlaThrProThrArgSerValAlaLysValThrThrArgLysHisGlnThrGlyValGl 195
Qy 745 GCCACCAGGAGAGCTCCAAAGGTATGTGAAGCTGCAGAAATAAAA 790
Db 195 uSerProHisArgAsnIleGlyPheValCysProValGlnLeuLys 210

RESULT 13
T31690
hypothetical protein F27E11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Mar-2001
C:Accession: T31690
R:Wamsley, P.; Keppler, D.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid F27E11.
A:Reference number: Z21069
A:Accession: T31690
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-605 *WAM*
A:Cross-references: EMBL:AF016413; PIDN:AAB65257.1; GSPDB:GN00023; CESP:F27E11.3
A:Experimental source: strain Bristol N2; clone F27E11
C:Genetics:
A:Gene: CESP:F27E11.3
A:Map position: 5
A:Introns: 28/3; 454/1; 520/1; 562/1
C:Superfamily: fruit fly frizzled protein

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Alignment Scores:			
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Score:	224.50	Matches:	42
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US-08-949-904A-1 (1-2027) x T31690 (1-605)			
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Qy	496	CCGCTGGTCATGAAGCAGGTGCCACCCGGACACCAAGAAGTTCCTGTCTCGCTCTTGGCC	555
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Qy	556	CCGCTGTGCTCGATGACCTAGACGAGACCATCAGCCATGCCACTCGCTCTGGGTGCAG	615
Db	45	ProIleCysGlnGluAsnTyrrAspLysProIleLeuProCysMetGluLeuCysValGlu	64
Qy	616	GTGAAGGACCGGTGCGCCCGGTCTATGCTCCGCTTTCCTCGTCCGCCCGACATGCTT	675
Db	65	AlaArgSerLysCysSerProIleMetAlaLysTyrrGlyPheAsgTrrProGluThrLeu	84
Qy	676	GATGGCAGCGTTTCCCCAGACAAACACCTTTGTCATCCCTCGCTAGCAGGACCAC	735
Db	85	SetCysGluAlaLeuProLysMetSerAsp	100
Qy	736	CTCCTGCGACCAACCCAGAGAAGCTCCAAAGGTATGTGAAGCC	786

Db	101	IleCysAlaAlaProAspThrProLysLysGlnHisLysGlyHisHisLysAsn	120	::: ::::
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RESULT 14				
JB0315				
low-density lipoprotein receptor-related protein - mouse				
C/Species: Mus musculus (house mouse)				
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004				
C/Accession: JE0315				
R/Tomita, Y.; Kim, D.; Magoori, K.; Fujino, T.; Yamamoto, T.T.				
J. Biochem. 124, 784-789, 1998				
A/Title: A novel low-density lipoprotein receptor-related protein with type II membrane				
A/Reference number: JE0315; MUID:98429596; PMID:9756624				
A/Accession: JE0315				
A/Status: preliminary				
A/Molecule type: mRNA				
A/Residues: 1-1113 <TOM>				
A/Cross-references: UNIPROT:Q92319; DDBJ:AB013874; NID:G3869144; PIDN:BAA34371.1; PID:G3				
C/Superfamily: mouse low-density lipoprotein receptor-related protein; LDL receptor lig				
F/337-372/Domain: LDL receptor ligand-binding repeat homology <LDL1>				
F/374-408/Domain: LDL receptor ligand-binding repeat homology <LDL2>				
F/410-445/Domain: LDL receptor ligand-binding repeat homology <LDL3>				
F/447-482/Domain: LDL receptor ligand-binding repeat homology <LDL4>				
F/648-682/Domain: LDL receptor ligand-binding repeat homology <LDL5>				
F/684-720/Domain: LDL receptor ligand-binding repeat homology <LDL6>				
F/723-757/Domain: LDL receptor ligand-binding repeat homology <LDL7>				
F/869-1097/Domain: trypsin homology <TRY>				
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Query Match:	6.15%	Indels:	27	
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US-08-949-904A-1 (1-2027) x JB0315 (1-1113)				
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QY	367	AGCAATTGCAAGCCCATCCGGCCCACTCCAGCTGTGCCACGGCATCGAATACCAGAAC	426	::: ::::
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QY	427	ATCGCGGTGCCCACTGCTGGGCCAGACCATGAAGGAG-----GTGCTGGAGCAG	480	::: ::::
Db	539	ThrHisTyrProAsnTyrLeuGlyHisArgThrGlnLysGluAlaSerIleSerTrpGlu	558	::: ::::
QY	481	CGCGCGCTTGGATCCCGCTGGTCATGAACAGCATGCCCCCGGACACCAAGAGTTCCTG	540	::: ::::
Db	559	SerSerLeuPheProAlaLeuValGlnThrAsnCysTyrLysTyrLeuMetPhePheAla	578	::: ::::
QY	541	TGCTCGCTTTCGCCCGCCGCTCGCTCGATGACATGACAGACCATCCAGCCATGCCAC	600	::: ::::
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QY	601	TCGCTCTGCTGAGGTGAGGACCGCTGCGCCCGGTGTCATGTCGCGCTTCGCGCTCCCC	660	::: ::::
Db	599	LeuLeuCysGluHisSerLysGluArgCysGluSerValLeuGlyLeValGlyLeuGln	618	::: ::::
QY	661	TGGCCCGACATGCTTGAGTCGACCGCTTTCGCCAG-----GACAAACGACCTTTCG	711	::: ::::
Db	619	TrpProGluAspThrAspCysAsnGlnPheProGluGluSerSerAspAsnGlnThrCys	638	::: ::::
QY	712	ATCCCCCTCTGCTAGCAGCGACCACTCTCTGCCAGCCACCGAGGAAGCTCCAAAGGTATGT	771	::: ::::
Db	639	Leu-----LeuProAsnGluAsp-----ValGluCysSerProSerHis	652	::: ::::

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: September 1, 2005, 09:39:32 ; Search time 631.5 Seconds
(without alignments)
2528.202 Million cell updates/sec

Title: US-08-949-904A-1
Perfect score: 3585
Sequence: 1 GAATTCGGCCTTCATGGCCT.....AAAAAAAAAAGCGCGCGC 2027

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 3548624

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Published Applications AA -QWMSfastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1976.5	55.1	377	14	US-10-106-698-6382	Sequence 6382, App
2	1594	44.5	295	8	US-08-949-904-2	Sequence 2, Appli
3	1594	44.5	295	14	US-10-177-293-142	Sequence 142, App
4	1594	44.5	295	15	US-10-295-027-1345	Sequence 1345, Ap
5	1594	44.5	295	16	US-10-783-528-107	Sequence 107, App
6	1594	44.5	295	17	US-10-847-972-78	Sequence 78, Appl
7	1594	44.5	295	17	US-10-432-256-2	Sequence 2, Appli
8	1590	44.4	295	9	US-09-978-295A-415	Sequence 415, App
9	1590	44.4	295	9	US-09-978-697-415	Sequence 415, App
10	1590	44.4	295	9	US-09-978-192A-415	Sequence 415, App
11	1590	44.4	295	9	US-09-999-832A-415	Sequence 415, App
12	1590	44.4	295	10	US-09-978-189-415	Sequence 415, App
13	1590	44.4	295	10	US-09-978-608A-415	Sequence 415, App
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ALIGNMENTS

RESULT 1
US-10-106-698-6382
; Sequence 6382, Application US/10106698
; Publication No. US20030103690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10106.698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8584
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6382
; LENGTH: 377

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (127)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6382

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Alignment Scores:	
Pred. No.:	1.31e-127
Score:	1976.50
Percent Similarity:	98.93%
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Query Match:	55.13%
DB:	14
Length:	3
Matches:	3
Conservative:	0
Mismatches:	0
Indels:	2
Gaps:	1

US-08-949-904A-1 (1-2027) x US-10-106-698-6382 (1-377)

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64	Db	oProArgProSerProAlaProLeuProLeuProProArgGlyArgAlaProThrMetLe	84
261	QY	CGAGGGCCCTGCTCGCTGCTGCTCTTCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCGC	320
84	Db	uGlnGlyProGlySerLeuLeuLeuLeuPheLeuAlaSerHisCysLeuGlySerAl	104
321	QY	CGCGGGCTTCTCTCTTTGGCCAGCCGACTTCTCTCAAGCGCAGCAATTCGAAGCC	380
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144	Db	nLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIleProLe	164
501	QY	GTCATGAAGAGTGCACCCGCGACACAAGAAAGTTCTGTGCTCGCTCTTCCGCCCGCT	560
164	Db	uValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAlaProA	184
561	QY	CTGCTCTGCATGACTAGACGAGACCATCCAGCCATGCCACTCGCTCTGCTGCGAGTGA	620
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621	QY	GGACCGCTGCGCGCGGTTCATGTCGCGCTTCGGCTTCCTCCCTGCGCCGACATGCTT	680
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Qy	861	GATAACCTTCATCAACACCGAGATACCAAAATCATCTCGGAGACCAAGACGACCAATTTA	920
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; Sequence 2, Application US/08949904			
; Publication No. US20030175855A1			
; GENERAL INFORMATION:			
; APPLICANT: LaVallie, Edward			
; APPLICANT: Racie, Lisa			
; TITLE OF INVENTION: HUMAN SDF-5 PROTEIN AND COMPOSITIONS			
; NUMBER OF SEQUENCES: 6			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: GENETICS INSTITUTE, INC.			
; STREET: 87 CAMBRIDGE PARK DRIVE			
; CITY: CAMBRIDGE			
; STATE: MA			
; COUNTRY: USA			
; ZIP: 02140			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/949,904			
; FILING DATE: October 15, 1997			
; CLASSIFICATION: 536			
; ATTORNEY/AGENT INFORMATION:			
; NAME: LAZAR, STEVEN R.			
; REGISTRATION NUMBER: 32,618			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (617) 498-8260			
; TELEFAX: (617) 876-5851			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 295 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-949-904-2			
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Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 44.46% Indels: 0			
DB: 8 Gaps: 0			
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221	Db	221	IleTyrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys	240
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; Sequence 1345, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynnne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-01250005
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1

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; Sequence 2, Application US/10432256
; Publication No. US20050113291A1
; GENERAL INFORMATION:
; APPLICANT: Applied Research Systems ARS Holding N.V.
; TITLE OF INVENTION: Use of SARP-1 in the treatment and/or prevention of scleroderma
; FILE REFERENCE: EP 469 Y
; CURRENT APPLICATION NUMBER: US/10/432,256
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-432-256-2

Alignment Scores:
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.46% Indels: 0
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US-08-949-904A-1 (1-2027) x US-10-432-256-2 (1-295)

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; Sequence 415, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
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Alignment Scores:		
Pred. No.:	5.35e-101	Length:
Score:	1590.00	Matches:
Percent Similarity:	99.66%	Conservative: 0
Best Local Similarity:	99.66%	Mismatches: 1
Query Match:	44.35%	Indels: 0
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Db 61 ProAsnLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80
Qy 496 CGCTGGTTCATGAAGCAGTGCACCGGACACCAAGAGTTCCTGTGCTCGCTCTTCGCC 555
Db 81 ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla 100
Qy 556 CCCGTCTGCTCGATGACCTAGACGAGACCATCCAGCCATCGCTCGCTCTCGCTGCAG 615
Db 101 ProValCysLeuAspAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120
Qy 616 GTGAGGACCGCTGGCGCCCGCTCATGTCCGGCTTCCTCGGCTTCCCTGGCCGACATGCTT 675
Db 121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140
Qy 676 GAGTGGACCGTTTCCCGGACGACACGACCTTTCATCCCTCGCTAGCAGCGACACAC 735
Db 141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160
Qy 736 CTCCTGCCACGCCAGGAGCTCCAAAGGTATGTGAAGCTCGCTGCAAAATAAAAAATGAT 795
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Qy 796 GATGACAGCACATATGAAACGCTTTGTAAATAATGATTTTGCACTGAAATAAAAGTG 855
Db 181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200
Qy 856 AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTCGAGACCAAGCAAGACC 915
Db 201 LysGluIleThrTyrIleAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr 220
Qy 916 ATTTCAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAAATCGGTGTGTGGCTCAAA 975
Db 221 IleTyrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys 240
Qy 976 GACAGCTTCAGTGACCTGTGAGAGATGAACGACATCAACGCGCCCTATCTGTCTATG 1035
Db 241 AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrLeuValMet 260
Qy 1036 GGACAGAAACAGGGTGGGAGCTGTGTACCTCGGTGAACGGTGGCAGAGGGGCGAG 1095
Db 261 GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln 280
Qy 1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140
Db 281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys 295

RESULT 12

US-09-978-189-415
; Sequence 415, Application US/09978189
; Publication No. US20030004102A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Hillan, Kenneth J.
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; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085697

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Query Match: 44.35% Indels: 0
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US-08-949-904A-1 (1-2027) x US-09-978-189-415 (1-295)

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QY 316 TCGGGCGCGGGCTCTCTCTTTGGCCAGCCCGACTTCTCTCAAGCGAGCAATTGC 375
|||
Db 21 SerAlaArgGlyLeuPheLeuPheGlyGlnProaspPheSerTyFLysArgSerAsnCys 40
QY 376 AAGCCCATCCCGGCCAACCTGCAGCTGTGCCACGGCATCGAATACCAGAACATCGGGCTG 435
|||
Db 41 LysProIleProValAsnLeuGlnLeuCysHISGlyIleGluTyTGlnAsnMetArgLeu 60
QY 436 CCCAACCTGCTGGGCCACGACACCATGAAGAGGTGTGGAGCAGCGCGCGCTTGGATC 495
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Db 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80
QY 496 CGCTGTGTCATGAGCAGTGCACCCGACACCAAGAGATTTCCTGTGCTCGCTCTTCGCC 555
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Db 81 ProLeuValMetLysGlnCysHisProaspThrLysLysPheLeuCysSerLeuPheAla 100
QY 556 CCCGTCTCGCTCGATGACCTAGACGAGACCATCGACCATCGCTCTCGCTGCTGCGCAG 615
|||
Db 101 ProValCysLeuAspAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120
QY 616 GTGAAGGACCGCTGCGCCCGGTGATGTCGCCCTTCGGCTTCGCCCTGCCCGACATGCTT 675
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Db 121 VallysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProaspMetLeu 140
QY 676 GAGTGGGACCGTTTCCCCCAGGACAAACGACCTTTTGCATCCCCCTCGCTAGCAGCGACCAC 735

141	Db	GlucyAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis	160
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796	Qy	GATGACAAACACATAAATGGAAACGCTTTGTAAAAATGATTTTGACACTGAAAAATAAAAGTG	855
181	Db	AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal	200
856	Qy	AAGGAGATAACCTTACATCAACCGAGATACCAAATCATCTCTGGAGACCAAGACGACGACC	915
201	Db	LysGluIleThrTyrlleAsnArgAspThrLysIlelleLeuGluThrLysSerLysThr	220
916	Qy	ATTTCACAGCTGAACGGTGTGTCGGAAGGGACCTGAAGAATCGGTGCTGTGGCTCAAA	975
221	Db	IleTyrlLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys	240
976	Qy	GACAGCTTGAGTGTCACCTGTGAGGAGATGAACGACATCAACGGCGCCCTATCTGGTCA TG	1035
241	Db	AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrlLeuValMet	260
1036	Qy	GGACAGAAAAACAGGCTGGGGAGCTGGTGATCACCTCGGTGAAGCGGCTGGCAGAAAGGGCAG	1095
261	Db	GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln	280
1096	Qy	AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC	1140
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RESULT 13

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US-0978-608A-415
; Sequence 415, Application US/09978608A
; Publication No. US20030045462A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 415
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; TYPE: PRT

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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 1, 2005, 09:26:23 ; Search time 51 Seconds
(without alignments)
5933.869 Million cell updates/sec

Title: US-08-949-904A-1

Perfect score: 3585

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1586	44.2	296	4	US-09-148-545-237 Sequence 237, Appl
3	1557	43.4	295	4	US-08-937-067-2 Sequence 2, Appli
4	1140	31.8	212	4	US-08-937-067-4 Sequence 4, Appli
5	624	17.4	317	4	US-08-937-067-6 Sequence 6, Appli
6	624	17.4	317	4	US-09-949-016-6300 Sequence 6300, Ap
7	614.5	17.1	305	4	US-09-949-016-7706 Sequence 7706, Ap
8	608	17.0	313	4	US-09-514-885-1 Sequence 1, Appli
9	608	17.0	313	4	US-09-949-016-6299 Sequence 6299, Ap
10	606.5	16.9	314	4	US-08-937-067-7 Sequence 7, Appli
11	606	16.9	313	4	US-09-546-043-3 Sequence 3, Appli
12	606	16.9	338	4	US-09-546-043-4 Sequence 4, Appli

ALIGNMENTS

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; Sequence 179, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
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; EARLIER APPLICATION NUMBER: 60/047,502
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EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 237

ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-937-067-6

Alignment Scores:
Pred. No.: 1.18e-43 Length: 317
Score: 624.00 Matches: 132
Percent Similarity: 57.01% Conservatives: 51
Best Local Similarity: 41.12% Mismatches: 97
Query Match: 17.41% Indels: 41
DB: 7 Gaps: 4

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Qy	456	GAC	CATGA	AGGAGTGTGG	AGCAGCGCGCTTGGATCCGCTGGTCATGAAGCAGTG	515
Db	80	u	Ser	Leu	Ala	Glu
Qy	516	CA	CCCGGAC	CAACAGAA	GTCTTCTGCTCTTTCGCGCCCGCTGCTGATGACCT	575
Db	100	s	His	Ser	Asp	Thr
Qy	576	AG	ACGAG	ACATCC	ACCTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGGCC	635
Db	117	u	Asp	Arg	Pro	Leu
Qy	636	GT	CATGTC	CGGCTTCC	CTCGCGCCGACATGCTTGA	TGCGGACCGTTTCCCCCA
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US-08-949-904A-1 (1-2027) x US-09-949-016-6300 (1-317)

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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-937-067-6

Alignment Scores:
Pred. No.: 1,18e-43 Length: 317
Score: 624.00 Matches: 132
Percent Similarity: 57.01% Conservatives: 51
Best Local Similarity: 41.12% Mismatches: 97
Query Match: 17.41% Indels: 41
DB: 7 Gaps: 4

US-08-949-904A-1 (1-2027) x US-08-937-067-6 (1-317)

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Db	100	s	His	Ser	Arg	Thr	Gln	Val	Phe	Leu	Cys	Ser	117
Qy	576	AG	ACGAG	ACAC	CCAC	CGAC	CTCG	CTCTG	CGCTG	CGAG	TGA	AGG	635
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Qy 1027 CTGCTCATGGACAGACAAACAGGGTGGGAGCTGGTGATCACCTCGGTGAAGCGGTGGCAG 1086
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; Sequence 1, Application US/09514885
; Patent No. 6556461
; GENERAL INFORMATION:
; APPLICANT: D'Armiesto, Jeanine
; APPLICANT: Imai, Kazuohi
; TITLE OF INVENTION: NOVEL THERAPEUTIC TREATMENT OF CHRONIC OBSTRUCTIVE
; PULMONARY DISEASE
; FILE REFERENCE: 58483.8pp
; CURRENT APPLICATION NUMBER: US/09/514,885
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Human
US-09-514-885-1

Alignment Scores:
Pred. No.: 2,53e-42 Length: 313
Score: 608.00 Matches: 123
Percent Similarity: 59.16% Conservative: 61
Best Local Similarity: 39.55% Mismatches: 107
Query Match: 16.96% Indels: 20
DB: 4 Gaps: 6

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Qy 328 CTCTTCCTTTGGCAGCCCGACCTCTCTACAGCGCAGCAATTGCAAGCCCATCCCG 387
Db 44 ProTyrGlnSerGlyArg-----PheTyrThrLysProGlnCysValAspIlePro 61
Qy 388 GCCAACCTGCAGCTGTGCCACCGCATACCAACATCGCGTGGCCCACTGCTG 447
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; Sequence 6299, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6299
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6299
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Alignment Scores:

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Pred. No.: 2,53e-42 Length: 313
Score: 608.00 Matches: 123
Percent Similarity: 59.16% Conservative: 61
Best Local Similarity: 39.55% Mismatches: 107
Query Match: 16.96% Indels: 20
DB: 4 Gaps: 6
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US-08-949-904A-1 (1-2027) x US-09-949-016-6299 (1-313)

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Qy 241 GGTGGCGGCCACCATGCTGTCAGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 4 GlyArgSerGluGlyGlyArgGlyAlaLeuGlyValLeuLeuAlaLeuGlyAlaAla 23
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QY 301 CACTGCTGCTGGCTCGCGCGC-----GGG 327
Db 24 LeuLeuAlaValGlySerAlaSerGluTyrAspTyrValSerPheGlnSerAspIleGly 43
QY 328 CTCCTCCCTTTGGCGCAGCCGACTTCTCTACAGCGCAGCAATTGCAAGCCCATCCCG 387
Db 44 ProTyrGlnSerGlyArg-----PheTyrThrLysProGlnCysValAspIlePro 61
QY 388 GCCAACCTGCAGCTGTGCCAGCGCATCGAATACCAAGACATCGCGCTGCCCAACCTGCTG 447
Db 62 AlaAspLeuArgLeuCysHisAsnValGlyTyrLysLysMetValLeuProAsnLeuLeu 81
QY 448 GCCACGAGACCATGAAGAGGTGCTGGAGCGAGCGCGGCTTGATCCCGCTGTGTCATG 507
Db 82 GluHisGluThrMetAlaGluValLysGlnGlnAlaSerSerTrpValProLeuLeuAsn 101
QY 508 AAGCAGTGCACCGGACACCAAGATTCTCGTCTGCTCGCTTCCGCCCGCTGCTGCTC 567
Db 102 LysAsnCysHisAlaGlyThrGlnValPheLeuCysSerLeuPheAlaProValCys--- 120
QY 568 GATGACCTAGACGAGACCATCGACCATCGCTCGCTGCTGCGTGCAGGTGAAGACCGC 627
Db 121 -----LeuAspArgProIleTyrProCysArgTrpLeuCysGluAlaValArgAspSer 138
QY 628 TGGCGCCCGGTGATGCGCCCTTCCGCTTCCCTGCGCGAGCATGCTTGAGTGCGACCGT 687
Db 139 CysGluProValMetGlnPhePheGlyPheTyrTrpProGluMetLeuLysCysAspLys 158
QY 688 TTCCTCCCGGACCAAGCCTTTGTCATCCCTCCCTGCTAGCAGGACCATCTCTGCGCAGCC 747
Db 159 PhePro---GluGlyAspValCysIleAlaMetThrProProAsnAlaThrGluAlaSer 177
QY 748 ACCGAGGAGCTCCAAAGGTATGTGAAGCTGCTCAAAATATAAAATGATGATGACCAACGAC 807
Db 178 LysProGlnGlyThrThrValCysProProCysAspAsnGluLeuLysSerGlu---Ala 196
QY 808 ATATGGAAACCTTTGTAATAATGATTTTGACTGAAATAATAAGTGAAGAGATAACC 867
Db 197 IleIleGluHisLeuCysAlaSerGluPheAlaLeuArgMetLysIleLysGluValLys 216
QY 868 TATACCAACCGAGATACCAAAATCATCTGGAGACCAAGACAGCAACCATTTTACAGCTG 927
Db 217 LysGluAsnGlyAspLysIleVal-----ProLysLysLysLysProLeuLysLeu 234
QY 928 AACGGTGTGTCGAAAGGACCTGAAGAAATCGTGTGCTGCTCAAAAGACAGCTTGCAG 987
Db 235 GlyProIleLysLysAspLeuLysLysLeuValLeuTyrLeuLysAsnGlyAlaAsp 254
QY 988 TGCACCTGTGAGGAGATGAACACATCAACGCGCCCTATCTGGTCATGGGACAGAAACAG 1047
Db 255 CysProCysHisGlnLeuAspAsnLeuSerHisHisPheLeuIleMetGlyArgLysVal 274
QY 1048 GTTGGGGAGCTGTGATCACCCTCGTGAAGCGGTGCGAGAGGGGCGCAGAGAGTTCAAG 1107
Db 275 LysSerGlnTyrLeuLeuThrAlaIleHisLysTrpAspLysLysAsnLysGluPheLys 294
QY 1108 CGCATCTCCCGCAGCATCGCAAGCTGCAGTGC 1140
Db 295 AsnPheMetLysLysMetLysAsnHisGluCys 305

RESULT 10
US-08-937-067-7
; Sequence 7, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
; APPLICANT: Unanaky, Samuil
; APPLICANT: Melkonyan, Hovsep
; TITLE OF INVENTION: A FAMILY OF GENES ENCODING
; TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
```

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; ADDRESSEE: MORRISON & FOEBSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,067
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20018.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-937-067-7

Alignment Scores:
Pred. No.: 3,37e-42 Length: 314
Score: 606.50 Matches: 124
Percent Similarity: 58.65% Conservative: 59
Best Local Similarity: 39.74% Mismatches: 102
Query Match: 16.92% Indels: 27
DB: 4 Gaps: 7

US-08-949-904A-1 (1-2027) x US-08-937-067-7 (1-314)
QY 238 CGGGGTCTTCCTTTGGCCAGCATGCTGCGCGCCCTGCTGCTGCTGCTGCTGCTCTCTCTCGCC 297
Db 11 ArgGlyAlaAlaLeuGlyValLeuLeuAlaLeuGlyAlaAlaLeuLeu----- 26
QY 298 TCGCACTGCTGCTGCGCTCGCGCGC----- 324
Db 27 -----AlaValGlySerAlaSerGluTyrAspTyrValSerPheGlnSerAspIle 43
QY 325 GGGCTCTTCCTTTGGCCAGCCCGGACTTCTCTACAGCGCAGCAATTGCAAGCCCATC 384
Db 44 GlyProTyrGlnSerGlyArg-----PheTyrThrLysProGlnCysValAspIle 61
QY 385 CCGGCCCAACCTGCAGCTGTGCCAGCGCATCCGAATACCAAGAACATCGCGCTGCCCAACCTG 444
Db 62 ProAlaAspLeuArgLeuCysHisAsnValGlyTyrLysLysMetValLeuProAsnLeu 81
QY 445 CTGGGCCACGAGACCATGAAGAGGTGCTGGAGCGCGCGGCTTGATCCCGCTGTGTC 504
Db 82 LeuGluHisGluThrMetAlaGluValLysGlnGlnAlaSerSerTrpValProLeuLeu 101
QY 505 ATGAGCAGTGCACCGCGGACACCAAGATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
Db 102 AsnLysAsnCysHisAlaGlyThrGlnValPheLeuCysSerLeuPheAlaProValCys 121
QY 565 CTCGATGACCTAGACGAGACCATCCAGCATCCCATCGCTGCTGCTGCTGCTGCTGCTGCTG 624
Db 122 -----LeuAspArgProIleTyrProCysArgTrpLeuCysGluAlaValArgAsp 138
QY 625 CGCTGCGCCCGGTGATGCTGCGCTTCCGCTTCCCTGCGCCCGACATGCTTGAGTGCGAC 684
Db 139 SerCysGluProValMetGlnPhePheGlyPheTyrTrpProGluMetLeuLysCysAsp 158
QY 685 CGTTTCCCGGACGACCATCTTGTGATCCCTCGCTAGCAGGACCATCTCTCTGCGCA 744
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US-08-949-904A-1 (1-2027) x US-09-546-043-4 (1-338)
; FILE REFERENCE: 11613.13US11
; CURRENT APPLICATION NUMBER: US/09/087,031E
; CURRENT FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/087,031
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/050,417
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 24
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-087-031E-24
Alignment Scores:
Pred. No.: 5,37e-41 Length: 113
Score: 590.00 Matches: 105
Percent Similarity: 93.81% Conservative: 1
Best Local Similarity: 92.92% Mismatches: 7
Query Match: 16.46% Indels: 0
DB: 4 Gaps: 0
US-08-949-904A-1 (1-2027) x US-09-087-031E-24 (1-113)
QY 373 TGCAGAGCCATCCCGGCCAACCTGCGAGCTGTGCGACCGCATCGAATACCAAGACATGCGG 432
Db 1 CysLysProIleProAlaAsnLeuGlyLeuCysHisGlyIleGluTyrGlyAsnMetArg 20
QY 433 CTGCCAACCTGCTGGGCCACGAGACCATGAAGAGGTGCTGGAGAGCGCGCTTGG 492
Db 21 LeuProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlyAlaGlyAlaTrp 40
QY 493 ATCCCGCTGTGTCATGAAGACAGTGCACCGCACCAAGAGTTCCTGTCTCGCTCTTC 552
Db 41 IleProLeuValMetLysGlyCysHisProAspThrLysLysPheLeuCysSerLeuPhe 60
QY 553 GCCCGCTGCTCGCTCGATGACCTAGACAGACCATCAGCCATGCCACTCGCTCGGTG 612
Db 61 AlaProValCysLeuAspAspLeuAspGluThrIleGlyProCysHisSerLeuCysMet 80
QY 613 CAGGTGAAGGACCGCTGCGCCCGCTGATGTCGCTTCGCGCTTCCTGCGCCGACATG 672
Db 81 GlyValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMet 100
QY 673 CTTGAGTGGACCGCTTCCCGCAGGACCAACGACTTTGC 711
Db 101 LeuGluCysAspArgPheProGlyAspAsnAspLeuCys 113
RESULT 14
US-09-087-031E-4
; Sequence 4, Application US/09087031E
; Patent No. 6479255
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
; FILE REFERENCE: 11613.13US11
; CURRENT APPLICATION NUMBER: US/09/087,031E
; CURRENT FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/087,031
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/050,417
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-087-031E-4
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US-08-949-904A-1 (1-2027) x US-09-546-043-4 (1-338)
QY 271 GGCCTGCTGCTGCTCTTCTCGCTCGCACTGCTGCTGGGCTCGCGCGCGGCTC 330
Db 16 GlyValLeuAlaLeuGlyGlyAlaSerGlyArgGlyLeuGlySerGluTyrAspTyr 35
QY 331 TTCCTCTTTGGCCAGCCGAC-----TTCTCCTACAGCGC 366
Db 36 ValSerPhe---GlnSerAspIleGlyProTyrGlnSerGlyArgPheTyrThrLysPro 54
QY 367 AGCAATTGCAAGCCCATCCGCGCAACCTGCGAGCTGTGCCAGCATCGAATACCAAGAC 426
Db 55 ProGlnCysValAspIleProAlaAspLeuArgLeuCysHisAsnValGlyTyrLysLys 74
QY 427 ATGCGGCTGCCAACCTGCTGGGCCACGAGACCATGAAGGAGGTGCTGGAGAGCGCGC 486
Db 75 MetValLeuProAsnLeuLeuGluHisGluThrMetAlaGluValLysGlnAlaSer 94
QY 487 GCTTGGATCCCGTGTGATGAAGAGTGCACCCCGGACCAAGAGTTCCTGTGCTCG 546
Db 95 SerTrpValProLeuLeuAsnLysAsnCysHisAlaGlyThrGlnValPheLeuCysSer 114
QY 547 CTCCTCGCCCGCTGCTGCTCGATGACCTAGACGAGACCATCCAGCCACTCGCTCGCTC 606
Db 115 LeuPheAlaProValCys-----LeuAspArgProIleTyrProCysArgTrpLeu 131
QY 607 TGCCTGAGGTGAAGACCGCTGCGCCCGGTGTCGCTGCGCTTCGCTTCGCGTTCGCGCC 666
Db 132 CysGluAlaValArgAspSerCysGluProValMetGlnPhePheGlyPheTyrTrpPro 151
QY 667 GACATGCTGAGTGGACCGTTCCTCCCGAGGACAGCACTTTGATCCCTCGCTAGC 726
Db 152 GluMetLeuLysCysAspLysPhePro---GluGlyAspValCysIleAlaMetThrPro 170
QY 727 AGCGACCACTCTCTGCCGCCACCGAGGAGTCCAAAGGTATGTGAAGCTGCAAAAT 786
Db 171 ProAsnAlaThrGluAlaSerLysProGlnGlyThrValCysProCysAspAsn 190
QY 787 AAAAAATGATGATGACAAACGACATAATGGAACCGTTTGTAAATAATGATTTGCACTGAAA 846
Db 191 GluLeuLysSerGlu---AlaIleIleGluHisLeuCysAlaSerGluPheAlaLeuArg 209
QY 847 ATAAAGTGAAGAGATACCTACATCAACCGAGATACCAAAATCATCTCTGAGACCAAG 906
Db 210 MetLysIleLeuGluValLysLysGluAsnGlyAspLysLysIleVal-----ProLys 227
QY 907 AGCAAGACCATTTACAAGCTGAACCGTGTGTCGGAAGGACCTCGAAGAAATCGTGTGTG 966
Db 228 LysLysLysProLeuLysLeuGlyProIleLysLysLysAspLeuLysLysValLeu 247
QY 967 TGGCTCAAGACAGCTTGCAGTGCACCTGTGTGAGAGATGAACGACATCAACGCGCCTAT 1026
Db 248 TyrLeuLysAsnGlyAlaAspCysProCysHisGlnLeuAspAsnLysSerHisPhe 267
QY 1027 CTGCTCATCGGACAGAAACAGCGGTGGGAGCTGTGATCACCTCGTGAAGCGGTGGAG 1086
Db 268 LeuIleMetGlyArgLysValLysSerGlnTyrLeuThrAlaIleHisLysTrpAsp 287
QY 1087 AAGGGCGCAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTCGAGTGC 1140
Db 288 LysLysAsnLysGluPheLysAsnPheMetLysLysMetLysAsnHisGluCys 305
RESULT 13
US-09-087-031E-24
; Sequence 24, Application US/09087031E
; Patent No. 6479255
; GENERAL INFORMATION:
; APPLICANT: Rubin, Jeffrey S.
; APPLICANT: Finch, Paul
; APPLICANT: Aaronson, Stuart
; APPLICANT: He, Xi
; TITLE OF INVENTION: HUMAN FRP AND FRAGMENTS THEREOF INCLUDING METHODS FOR USING THEM
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Db 161 Pro---GluGlyAspValCysIleA

DD T6T PTO---GUGUUYWVRNATCUTETENTMESTMPTO-----PTOAVIHTA 174

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QY 751 GAGGAAGCTCCAAAG-----GTATGTGAAGCCTGCACAAATAAATAATGAT 795
Db ||||| ||| ||||| ||| |||:|:|
175 ThrGluAlaSerLysProGlyThrThrValCysProCysAspAsnGluLeuLys 194
QY 796 GATGACACGACATAATGGAACGCTTTGTAAAAATGATTTTGCACCTGAAAAATAAAGTG 855
Db :|:|:| ||| ||||| :|:|:| ||||| :|:|:| ||||| :|:|:| |||||
195 SerGlu--AlaIleIleGluHisLeuCysAlaSerGluPheAlaLeuArgMetLysIle 213
QY 856 AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTCGAGACCAAGCAAGACC 915
Db |||||:|:| ||| ||| |||||:|:| ||| |||
214 LysGluValLysLysGluAsnGlyAspLysLysIleVal-----ProLysLysLys 231
QY 916 ATTTACAAGCTGAACGGTGTGCCGAAAGGACCTGAAGAAATCGGTGCTGGCTCAAA 975
Db ||||| ||| :|:|:|:|:| ||||| ||||| |||||:|:| |||||
232 ProLeuLysLeuGlyProIleLysLysLysAspLeuLysLeuValLeuTyrLeuLys 251
QY 976 GACAGCTTCAGTGCACCTGTGAGGAGATGAACGACATCAACGCGCCCTATCTGTCATG 1035
Db :|:| ||| ||| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
252 AsnGlyAlaAspCysProCysHisGlyLeuAspAsnLeuSerHisPheLeuIleMet 271
QY 1036 GGACAGAAACAGGGTGGGAGCTGGTGATCACCTCGGTGAACGGGTGGCAGAGGGGCAG 1095
Db ||||:|:| ||| :|:|:|:|:|:|:|:|:|:|:|:|:|
272 GlyArgLysValLysSerGlyTyrLeuLeuThrAlaIleHisLysTrpAspLysLysAsn 291
QY 1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140
Db :|:|:| ||||| ||| :|:|:|:|:|:|:|:|:|:|
292 LysGluPheLysAsnPheMetLysLysMetLysAsnHisGluCys 306

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Search completed: September 1, 2005, 09:41:11
Job time : 61 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 1, 2005, 09:26:23; Search time 286 Seconds
(without alignments)
5482.261 Million cell updates/sec

Title: US-08-949-904A-1
Perfect score: 3585
Sequence: 1 GAATTCGGCCTTCATGGCCT.....AAAAAAAAAAAGCGCGCGC 2027

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q/cn2_1/USPTO.spool_p/US08949904/runat_01092005_102611_21240/app.query.fasta_1.2183
-DB=A Geneseq -Qfmt=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US08949904 @CN_1_1_308 @runat_01092005_102611_21240 -NCRP=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1976.5	55.1	377	4 AAG75608	Aag75608 Human col
2	1957.5	54.6	408	2 AAY74087	Aay74087 Human pro
3	1594	44.5	295	2 AAW82588	Aaw82588 Human ATG
4	1594	44.5	295	2 AAW49082	Aaw49082 Homo sapi
5	1594	44.5	295	2 AAY06923	Aay06923 Human sec
6	1594	44.5	295	5 ABG31499	Abg31499 Human sec
7	1594	44.5	295	6 ABU55908	Abu55908 Human pro
8	1594	44.5	295	6 AAE34062	Aae34062 SARP 2 pr
9	1594	44.5	295	6 ABR47455	AbR47455 Breast ca
10	1594	44.5	295	7 ADF77693	Adf77693 Human ful

11	1594	44.5	295	7 ADN40027	Adn40027 Cancer/an
12	1594	44.5	295	8 ADN05090	Adn05090 Antipsoi
13	1594	44.5	295	8 ADR46694	Adr46694 Cancer-as
14	1590	44.4	295	2 AAY41748	Aay41748 Human PRO
15	1590	44.4	295	3 AAB44304	Aab44304 Human PRO
16	1590	44.4	295	5 ABB84861	Abb84861 Human PRO
17	1590	44.4	295	5 ABB95467	Abb95467 Human ang
18	1590	44.4	295	6 ABO25250	AbO25250 Novel hum
19	1590	44.4	295	6 ABU72256	Abu72256 Novel hum
20	1590	44.4	295	6 ABU84936	Abu84936 Human sec
21	1590	44.4	295	6 ABU61134	Abu61134 Human PRO
22	1590	44.4	295	6 ABU80403	Abu80403 Human sec
23	1590	44.4	295	6 ADA24954	Ada24954 Novel hum
24	1590	44.4	295	6 ABO19705	AbO19705 Novel hum
25	1590	44.4	295	6 ADA12615	Ada12615 Human sec
26	1590	44.4	295	6 ABO19596	AbO19596 Novel hum
27	1590	44.4	295	7 ADB73921	AdB73921 Human PRO
28	1590	44.4	295	7 ADB76637	AdB76637 Human PRO
29	1590	44.4	295	7 ADC44063	AdC44063 Human sec
30	1590	44.4	295	7 ADC61823	AdC61823 Human sec
31	1590	44.4	295	7 ADC63787	AdC63787 Human sec
32	1590	44.4	295	7 ADC66887	AdC66887 Human sec
33	1590	44.4	295	7 ADC69011	AdC69011 Human sec
34	1590	44.4	295	7 ADC63071	AdC63071 Human sec
35	1590	44.4	295	7 ADC68136	AdC68136 Human sec
36	1590	44.4	295	7 ADC41456	AdC41456 Human sec
37	1590	44.4	295	7 ADC67511	AdC67511 Human sec
38	1590	44.4	295	7 ADC62447	AdC62447 Human sec
39	1590	44.4	295	7 ADC42080	AdC42080 Human sec
40	1590	44.4	295	7 ADD10479	AdD10479 Human sec
41	1590	44.4	295	7 ADD11339	AdD11339 Human sec
42	1590	44.4	295	7 ADD37132	AdD37132 Human sec
43	1590	44.4	295	7 ADE49449	Ade49449 Human sec
44	1590	44.4	295	7 ADE35503	Ade35503 Human sec
45	1590	44.4	295	7 ADE16617	Ade16617 Human sec

ALIGNMENTS

RESULT 1
AAG75608
ID AAG75608 standard; protein; 377 AA.
XX AAG75608;
XX AC AAG75608;
XX DT 03-SEP-2001 (first entry)
XX DE Human colon cancer antigen protein SEQ ID NO:6372.
XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX KW colorectal carcinoma.
XX OS Homo sapiens.
XX PN WO200122920-A2.
XX PD 05-APR-2001.
XX PF 28-SEP-2000; 2000WO-US026524.
XX PR 29-SEP-1999; 99US-0157137P.
XX PR 03-NOV-1999; 99US-0163280P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI: 2001-235357/24.
XX DR N-PSDB; AAH35013.
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.

Claim 11; Page 7840-7842; 9803pp; English.

AAH32943 to AAH37195 and AAAG73514 to AAAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patient's own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAH77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922

Sequence 377 AA;

CC activity. The sequences are also useful in producing pharmaceutical
compositions for treatment of pancreatic tumors. AAY73814-Y74252
CC represent protein fragments encoded by the human pancreatic tumor cDNA
library derived expressed sequence tag (EST) sequences represented in
CC AAZ52850-Z53014
XX
SQ Sequence 408 AA;

Alignment Scores:
Pred. No.: 1,21e-159 Length: 408
Score: 1957.50 Matches: 372
Percent Similarity: 99.20% Conservatives: 0
Best Local Similarity: 99.20% Mismatches: 0
Query Match: 54.60% Indels: 3
DB: 2 Gaps: 1

US-08-949-904A-1 (1-2027) x AAY74087 (1-408)

QY 23 CTCATTCTGCTCCCGGGTCCGAGCCCGCGGAGTGGCGGGCTTGACGCGCTCG 82
DB 36 LeuileLeuLeuProArgValGlyAlaProArgSerCysAlaArgAlaCysSerAlaSer 55
QY 83 CCGCGCTCTCC---CGGTGTCGCTTCTCCGCGCCCGCGCGCCGCGCTCCGAGTTT 139
DB 56 ProAlaLeu-SerSerArgCysProAlaSerProArgProSerArgLeuProAlaPh 75
QY 140 TCGGGGCCCCGAGTCCGACCCAGCAAGAGAGCGGGCCCGGACAGCTCGAAGCTCCGCGC 199
DB 75 eArgGlyProGluSerHisProAlaArgAlaGlyProGlyGlnAlaArgThrProAl 95
QY 200 CGCTCGCCCTTCCCGGGTCCGCTTCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 259
DB 95 alaSerProProGlySerAlaProSerAlaProSerGlySerArgAlaHisAspAl 115
QY 260 TGCAGGGCCCTGCTCGCTGCTGCTTCTTCTCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 319
DB 115 alaGlyProThrLeuAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 135
QY 320 CGCGGGGCTTCTCTCTTTGGCCAGCCCGGAGTCTCTCTACAGCGCGCAGCAATTCGAGC 379
DB 135 yalaArgAlaLeuProLeuTriProAlaArgLeuLeuLeuGlnAlaGln-AlenCysLysP 155
QY 380 CATCCCGGCCAACCTGACGTGTGCCACGGATCGAATACAGAACATGCGGCTGCCCA 439
DB 155 roileProAlaAsnLeuGlnLeuCysHisGlyIleGluTyrGlnAsnMetArgLeuProAl 175
QY 440 ACTGCTGGGCCACGAGCAGCAGGAGGTGCTCGAGCAGCGCGCGCTTGGATCCCGC 499
DB 175 enLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTriPleProL 195
QY 500 TGGTCATGAGCAGTCCGACCCGAGCACCAGAGTTCCTGTGCTCGCTCTTCGCGCCCG 559
DB 195 euValMetLysGlnCysHisProArgThrLysLysPheLeuLeuCysSerLeuPheAlaProV 215
QY 560 TGTGCTCGATGACCTAGACGAGACATCCAGCCATGCGCTCTGCTGCGTGCAGGTGA 619
DB 215 aLysLeuAspLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGlnVal 235
QY 620 AGGACCGCTCGCGCGGCTCATGCTCGGCTTCGGCTTCCCTCGCGCCCGCATGCTTGA 679
DB 235 yAspArgCysAlaProValMetSerAlaPheGlyPheProTriProAspMetLeuGluC 255
QY 680 GCGACCGTTTCCCGCAGCAACAGCTTTTGATCCCTCCCTAGCAGCGACCACTCC 739
DB 255 yAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHisLeuL 275
QY 740 TCCAGCCACCGAGGAGCTCCAAAGGTATGTGAAGCTTCGCAAAATATAAATATGATG 799
DB 275 euProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAspA 295
QY 800 ACAACGACATATGAAAGCGCTTTGTAATAATGATTTCACATGAAATAAAGTGAAG 859
DB 295 pAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysValLysG 315

QY 860 AGATAACCTACATCAACCGAGATACCAAAATCATCTCGAGACCAAGACCAAGACCATTT 919
DB 315 luileThr-TyrIleAsnArgAspThrLysIlelleLeuGluThrLysSerLysThrIleT 335
QY 920 ACAAGCTGAACGGTGTGTCGAAAGGGACCTGAGAAATCGGTGCTGGCTCAAGACA 979
DB 335 yLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLysAspS 355
QY 980 GCTTCAGCTGCACCTGTGAGGAGATGAACGACATCAACGCGCCCTATCTGTCTATGGGAC 1039
DB 355 erLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTrpLeuValMetGlyG 375
QY 1040 AGAAACACGGTGGGAGCTGTGTATCACTCGGTGAACGGTGGCAGAGGGGCGAGAG 1099
DB 375 lnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGlnA-GG 395
QY 1100 AGTTCAACGGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140
DB 395 luPheLysArgIleSerArgSerIleArgLysLeuGlnCys 408

RESULT 3
AAW82588
ID AAW82588 standard; protein; 295 AA.
XX AAW82588;
AC
XX
DT 01-MAR-1999 (first entry)
XX
DE Human ATG-1622 protein.
XX
KW ATG-1622; SDF5; human; secreted ligand; 7-transmembrane receptor;
diagnosis; disease; screening; vaccine; inoculate; treatment; obesity;
heart disease; hypertension; kidney disease; insulin resistance;
lipodystrophy; diabetes; central nervous system; CNS; gene mapping;
linkage analysis.
XX
OS Homo sapiens.
XX
PN EP879887-A1.
XX
PD 25-NOV-1998.
XX
PF 14-MAY-1998; 98EP-00302809.
XX
PR 21-MAY-1997; 97US-0047251P.
XX
PR 13-JUN-1997; 97US-00874156.
XX
PA (SMITK) SMITHKLINE BEECHAM CORP.
XX
PI Hu E, Zhu Y;
XX
DR WPI; 1998-596879/51.
DR N-PSDB; AAV69384.
XX
New human secreted protein ATG-1622 polypeptide and polynucleotide -
useful as diagnostic reagents and for prevention and treatment of Central
Nervous System diseases and diabetes.
XX
PS Claim 11; Page 22-23; 28pp; English.
XX
This sequence represents the human ATG-1622 protein which is related to
human secreted ligands for 7-transmembrane receptors and similar to
murine SDF5. ATG-1622 polypeptides and polynucleotides are useful for
diagnosing susceptibility to diseases by detecting mutations in the ATG-
1622 gene and can diagnose diseases associated with ATG-1622 imbalance.
The polypeptides can be used to screen for agonists and antagonists which
can be used in treatment to activate or inhibit ATG-1622 activity. The
ATG-1622 polypeptide can be administered directly or as a vaccine to
inoculate against disease. Diseases which can be diagnosed, prevented or
treated by the ATG-1622 polypeptide or polynucleotides include heart
disease, hypertension, kidney diseases, obesity, insulin resistance,
lipodystrophy, diabetes and central nervous system (CNS) diseases. The


```
Db 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80
Qy 496 CCGCTGGTCATGAAGCAGTGCACCCGAGCACCAAGAGTCTCTGCTCGCTCTTCGGCC 555
Db 81 ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla 100
Qy 556 CCGCTGCTGCTGATGACCTAGACGAGACCATCCAGCCATGCCACTCGCTCTGCTGCGTGCAG 615
Db 101 ProValCysLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120
Qy 616 GTGAGGACCGCTGGCCCGCTGCTATGCTCGGCTTCGGCTTCCCTGGCCGACATGCTT 675
Db 121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140
Qy 676 GAGTGCAGCGTTTCCCGCAGACACGACCTTTGTCATCCCTCGCTAGCAGCAGCACAC 735
Db 141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160
Qy 736 CTCCTGCCAGCCAGGAGGAGCTCAAAAGGTATGTGAAGCTGCAAAATATAAAATGAT 795
Db 161 LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp 180
Qy 796 GATGACACGACATATGACAGCGCTTGTAAATGATTTTGCCTGACCTGAAATATAAGTG 855
Db 181 AspAspAsnAspIleMetGluThrLeuLysLysAsnAspPheAlaLeuLysIleLysVal 200
Qy 856 AAGGAGATAACCTACATCAACGAGATACCAAAATCATCTCGAGACCAAGCAAGACC 915
Db 201 LysGluIleThrTyrlleAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr 220
Qy 916 ATTTCAAGCTGAACGGTGTGTCGAAAGGACCTGGAAGAAATCGGTGCTGTGGCTCAA 975
Db 221 IleTyrlleLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys 240
Qy 976 GACAGCTTCAGTGCACCTGTGAGAGATGAACGACATCAACGCCCTATCTGTGTCATG 1035
Db 241 AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrlleValMet 260
Qy 1036 GCACAGAACAGGGTGGGAGCTGGTGATCACCTCGGTGAACGGTGGCAGAAAGGGCAG 1095
Db 261 GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln 280
Qy 1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140
Db 281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys 295
RESULT 11
ADN40027
ID ADN40027 standard; protein; 295 AA.
XX
AC ADN40027;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C397.
XX
KW Human: differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnery; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-0036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0334393P.
03-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0347211P.
10-JAN-2002; 2002US-0347349P.
08-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0356714P.
20-FEB-2002; 2002US-0359077P.
29-MAR-2002; 2002US-0368809P.
04-APR-2002; 2002US-0370110P.
12-APR-2002; 2002US-0372246P.
05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
22-JUL-2002; 2002US-0397775P.
22-JUL-2002; 2002US-0397845P.
09-SEP-2002; 2002US-0409450P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
PA
XX
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
XX WPI; 2003-468649/44.
DR N-PSDB; ADN39810.
XX
XX Determining the presence or absence of a pathological cell in a patient,
XX useful for diagnosing, prognosing or treating cancer, comprises detecting
XX a nucleic acid in a biological sample.
XX
XX Claim 12; SEQ ID NO C397; 1385pp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX whose expression is upregulated or downregulated in specific cancers or
XX other diseases such as angiogenic or fibrotic disorders, and to methods
XX of determining the presence or absence of a pathological cell in a
XX patient by detecting a nucleic acid at least 80% identical to those of
XX the invention or by detecting a polypeptide of the invention. The
XX invention also relates to expression vectors and host cells comprising a
XX nucleic acid of the invention; antibodies which specifically bind a
XX polypeptide of the invention; use of such antibodies for drug targeting;
XX and methods of screening for modulators of activity or expression of the
XX polypeptides and nucleic acids. The nucleic acids, polypeptides,
XX antibodies and methods are useful for diagnosing, prognosing and treating
XX cancer and other conditions such as psoriasis, ischaemia, heart disease,
XX atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
XX neovascularisation syndromes, scarring and uterine fibroids. They may
XX also be useful in wound healing and in contraception. The present
XX sequence represents a polypeptide of the invention.
XX
SQ Sequence 295 AA;
Alignment Scores:
Pred. No.: 2,44e-128 Length: 295
Score: 1594.00 Matches: 295
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 44.46% Indels: 0
DB: 7 Gaps: 0
US-08-949-904A-1 (1-2027) x ADN40027 (1-295)
Qy 256 ATGCTGACGGGCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGGC 315
Db 1 MetLeuGlnGlyProGlySerLeuLeuLeuPheLeuAlaSerHisCysCysLeuGly 20
Qy 316 TCGGCGCGCGGCTCTTCTCTCTTTGGCCAGCCCGACTTCTCTCTCAAGCGCAGCAATTGC 375
Db 21 SerAlaArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrlleArgSerAsnCys 40
Qy 376 AAGCCCATCCCGGCCAACCTGACGTGTGCCACGGCATCGAATACCAAGCAATCGGCTG 435
Db 41 LysProIleProAlaAsnLeuGlnLeuCysHisGlyIleGluTyrlleGlnAsnMetArgLeu 60
```

QY 436 CCCAACCTGCTGGCCACGAGACCATGAAGAGGTGCTGGAGCGCGCGCTTGGATC 495
DB 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80
QY 496 CCGCTGGTCATGAAGCAGTGCACCCGACACCAAGAGTTCCTGTGCTCGCTCTTCGCC 555
DB 81 ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla 100
QY 556 CCGCTGCTGCTGATGACCTAGACGAGACCATCCAGCCATGCCACTCGCTCTGCTGGAG 615
DB 101 ProValCysLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120
QY 616 GTGAGGACCGCTGGCCCGCTCATGTCCGCTTCGGCTTCCTCCCTGGCCGACATGCTT 675
DB 121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140
QY 676 GAGTGCAGCCGTTTCCCCCAGACACGACCTTTGTCATCCCCCTCGCTAGCAGCACAC 735
DB 141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160
QY 736 CTCCTGCGACCGAGAGCTCCAAAGGTATGTGAAGCTGTGAAGCTGCCAAAATAAATGAT 795
DB 161 LeuLeuProAlaThrGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp 180
QY 796 GATGACACGACATATGGAACGCTTGTGTAAAATGATTTTGCACCTGAAATAAAGTG 855
DB 181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200
QY 856 AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTCGAGACCAAGACGAC 915
DB 201 LysGluIleThrTyrrIleAsnArgAspThrLysIleLeuLeuGluThrLysSerLysThr 220
QY 916 ATTTCAAGCTGAACGGTGTGTCGGAAGGACCTCGAAGAAATCGGTGCTGGCTCAAA 975
DB 221 IleTyrrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys 240
QY 976 GACAGCTTCAGTCACCTGTGAGGAGATGAACGACATCAACGCCCTCATCTGCTCATG 1035
DB 241 AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrrLeuValMet 260
QY 1036 GCACAGAAACAGGGTGGGAGCTGTGTATCACCTCGGTGAAGCGGTGGCAGAGGGCAG 1095
DB 261 GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln 280
QY 1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGC 1140
DB 281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys 295

RESULT 12

ADN05090

ID ADN05090 standard; protein; 295 AA.

XX AC

ADN05090;

XX DT

XX 01-JUL-2004 (first entry)

XX DE

XX Antipsoriatic protein sequence #724.

XX KW

XX antipsoriatic; gene therapy; psoriasis; diagnosis.

XX OS

XX Homo sapiens.

XX PN

XX WO2004028479-A2.

XX PD

XX 08-APR-2004.

XX PF

XX 25-SEP-2003; 2003WO-US030907.

XX PR

XX 25-SEP-2002; 2002US-0414006P.

XX PA

XX (GETH) GENENTECH INC.

XX

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;

XX WPI; 2004-305105/28.

DR N-PSDB; ADN05089.

XX New PRO nucleic acid or polypeptide, useful for preparing a

PT pharmaceutical composition for diagnosing or treating psoriasis in a

PT mammal.

XX Claim 9; SEQ ID NO 1484; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for

CC treating psoriasis or a sequence having at least 80% identity to the

CC above sequences. The nucleic acid is useful for preparing a composition

CC for diagnosing or treating psoriasis in a mammal. This sequence

CC corresponds to one of the polypeptides of the invention.

XX Sequence 295 AA;

Alignment Scores:

Score: 2.44e-128 Length: 295

Percent Similarity: 1594.00 Matches: 295

Best Local Similarity: 100.00% Conservative: 0

Query Match: 44.46% Indels: 0

DB: 8 Gaps: 0

US-08-949-904A-1 (1-2027) x ADN05090 (1-295)

QY 256 ATGCTGACAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315

DB 1 MetLeuGlnGlyProGlySerLeuLeuLeuLeuPheLeuAlaSerHisCysCysLeuGly 20

QY 316 TCGCGCGCGCGCTTCTCTCTTTGGCAGCCCGACTTCTCCTCAAGCGCAGCAATGCG 375

DB 21 SerAlaArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrrLysArgSerAsnCys 40

QY 376 AAGCCCATCCCGGCCAACCTGCAGCTGTGCCAGGCATCGAATACCGAAGATCGGCTG 435

DB 41 LysProIleProAlaAsnLeuGlnLeuCysHisGlyIleGluTyrrGlnAsnMetArgLeu 60

QY 436 CCCAACCTGCTGGCGCCACGAGACCATGAAGAGAGTGTGGAGCAGCGCGCGCTTGAATC 495

DB 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80

QY 496 CCGCTGGTTCATGAAGCAGTGCACCCGACACCAAGAGTTCTGTGCTCGCTCTTCGCC 555

DB 81 ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla 100

QY 556 CCGCTGCTGCTGATGACCTAGACGAGACCATCCAGCCATGCCACTCGCTGCTGCTGAG 615

DB 101 ProValCysLeuAspAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120

QY 616 GTGAAGGACCGCTGCGCCCGCTCATGTCCGCTTTCGCTTCCCTGCGCCGACATGCTT 675

DB 121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140

QY 676 GAGTGCAGCCGTTTCCCCCAGGACCAAGACCTTTGTCATFCCCCCTCGCTAGCAGCAC 735

DB 141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160

QY 736 CTCCTGCGACCGAGAGCTCCAAAGGTATGTGAAGCTGTGAAGCTGCCAAAATAAATGAT 795

DB 161 LeuLeuProAlaThrGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp 180

QY 796 GATGACACGACATAATGGAACCGCTTGTAAAATGATTTTGGCACTGAAAATAAAGTG 855

DB 181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200

QY 856 AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTCGGAGACCAAGACGAC 915

DB 201 LysGluIleThrTyrrIleAsnArgAspThrLysIleLeuLeuGluThrLysSerLysThr 220

Db 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluGlnAlaGlyAlaTrpIle 80
QY 496 CCGCTGGTCATGAAGCAGTGCACCCCGAGCACCAAGAAGTTCTGTGCTCGCTCTTCGCG 555
Db 81 ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla 100
QY 556 CCGCTGCTGCTGATGACCTAGACGAGACATCCAGCCATGCCATCGCTCTGCTGCGTGCAG 615
Db 101 ProValCysLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120
QY 616 GTGAGGACCGCTGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
Db 121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140
QY 676 GAGTGCAGCGCTTCCCGCAGGACACGACCTTTGTCATCCCTCCCTAGCAGCAGCAC 735
Db 141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160
QY 736 CTCCTGCCAGCCAGGAGGCTCCAAAGGTATGTGAAGCTGCAAGCTGCAAAATATAAATGAT 795
Db 161 LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp 180
QY 796 GATGACACGACATATGAAACGCTTTCTGAAATGATTTTGCATGAAATATAAGTG 855
Db 181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200
QY 856 AAGGAGATACCTACATCAACGAGATACCAAAATCATCTCGAGACCAAGAGCAGACC 915
Db 201 LysGluIleThrTyrlleAsnArgAspThrLysIleIleGluThrLysSerLysThr 220
QY 916 ATTTCAAGCTGAACGGTGTGTCGAAAGCGACCTGAAAGAAATCGGTGCTGTGCTCAA 975
Db 221 IleTyrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys 240
QY 976 GACAGCTTCAGTGCACCTGTGAGNGATGAAGCATCAACGCGCCCTATCTGTGTCATG 1035
Db 241 AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrLeuValMet 260
QY 1036 GCAGACAAACAGGGTGGGAGCTGTGTGATCACCTCGTGAAGCGGTGGCAGAGGGCAG 1095
Db 261 GlyGlnLysGlnGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln 280
QY 1096 AGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCATGC 1140
Db 281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys 295
RESULT 15
ID AAB44304 standard; protein; 295 AA.
AC AAB44304;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO697 (UNQ361) protein sequence SEQ ID NO:415.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytosstatic;
KW expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US004341.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 29-MAR-1999; 99US-0126773P.
PR 21-APR-1999; 99US-0130232P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.

PR 23-JUN-1999; 99US-0141037P.
PR 26-JUL-1999; 99US-0145698P.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
XX (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrera N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI: 2000-611443/58.
DR N-PSDB; AAC78560.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.
XX
PS Claim 12; Fig 167; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
CC The PRO polynucleotides and polypeptides have cytostatic activity. The
CC polynucleotides and polypeptides can be used for detecting the presence
CC of PRO polypeptides in samples, for linking bioactive molecules to cells
CC and for modulating biological activities of cells, using the polypeptides
CC for specific targeting. The polypeptide targeting can be used to kill the
CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
CC provide specific targeting of bioactive molecules to cells. AAC78600 to
CC AAC78987 represent PCR primers and probes used in the isolation of the
CC PRO polynucleotide sequences
XX
SQ Sequence 295 AA;
Alignment Scores:
Pred. No.: 5,4e-128 Length: 295
Score: 1590.00 Matches: 294
Percent Similarity: 99.66% Conservative: 0
Best Local Similarity: 99.66% Mismatches: 1
Query Match: 44.35% Indels: 0
DB: 3 Gaps: 0
US-08-949-904A-1 (1-2027) x AAB44304 (1-295)
QY 256 ATGCTGCAGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCGC 315
Db 1 MetLeuGlnGlyProGlySerLeuLeuLeuLeuPheLeuAlaSerHisCysLeuGly 20
QY 316 TCGCGCGCGGGCTCTTCTCTTTGGCCAGCCCGCTTCTCTTCAAGCCGAGCAATTCG 375
Db 21 SerAlaArgGlyLeuPheLeuGlyGlnProAspPheSerTyrLysArgSerAsnCys 40
QY 376 AAGCCCATCCCGCCCAACCTGACGTGCGCAGCGCATCGAATACCGAAGCAATTCG 435
Db 41 LysProIleProValAsnLeuGlnCysHisGlyIleGluTyrGlnAsnMetArgLeu 60
QY 436 CCCAACCTGCTGGGCGCCACGACCATGAAGAGAGTGTGGAGCAGCGCGCTTGGATC 495
Db 61 ProAsnLeuLeuGlyHisGluThrMetLysGluValLeuGluAlaGlyAlaTrpIle 80
QY 496 CCGCTGGTTCATGAAGCAGTGCACCCGAGCACCAAGAAGTTCTGTGCTCGCTCTTCGCG 555
Db 81 ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla 100

QY 556 CCGCTCTGCCTCGATGACCTAGACGAGACCATCCAGCATGCCACTCGCTCTCGGTGCAG 615
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
101 ProValCysLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120
QY 616 GTGAAGGACCGCTGCGCCCGGTGTCATGTCGGCTTCGGCTTCCCTGGCCCGACATGCTT 675
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeu 140
QY 676 GAGTGCAGCGTTTCCCCCAGGACAAACGACCTTTGTCATCCCCCTCGCTAGCAGCGACCCAC 735
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160
QY 736 CTCCTGCCAGCCACGAGAGAGCTCCAAAGGTATGTGAAGCTTGCAGGCTGCAAAAATAAATGAT 795
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
161 LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp 180
QY 796 GATGACAAACGACATAATGAAACGCTTTGTAAAAATGATTTGCACATGAAAAATAAAAGTG 855
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200
QY 856 AAGGAGATACCTACATCAACCGAGATACCAAAATCATCTCGAGACCAAGAGCAAGACC 915
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
201 LysGluIleThrTyriLeAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr 220
QY 916 ATTTACAAGCTGAACGGTGTGTCGGAAGGGACCTGAAGAAATCGGTGCTGTGGCTCAA 975
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
221 IleTyrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys 240
QY 976 GACAGCTTCAGTGCACCTGTGAGGAGATGAACGACATCAACGCGCCCTATCTGGTTCATG 1035
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrLeuValMet 260
QY 1036 GGACAGAAAACAGGTGGGAGCTGGTGATCACCTCGGTGAACGGTGGCAGAAAGGGGCAG 1095
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
261 GlyGlnLysGlnGlyGlyGluLeuValIleThrSerValLysArgTrpGlnLysGlyGln 280
QY 1096 AGAGAGTTCAAGGCAATCTCCCGCAGCATCCGCAAGCTCGACGTGC 1140
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys 295

Search completed: September 1, 2005, 09:50:52
Job time : 300 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 09:51:02 ; Search time 118.518 Seconds
(without alignments)
1274.608 Million cell updates/sec

Title: US-08-949-904A-2

Perfect score: 1594

Sequence: 1 MLQPGSLLLLFLASHCCLG.....WQKQREPKRISIRKLQC 295

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1594	100.0	295	2 Q9HAP5	Q9HAP5 homo sapien
2	1590	99.7	295	2 Q9GHF1	Q9GHF1 homo sapien
3	1560	97.9	295	2 O08862	O08862 mus musculus
4	1557	97.7	295	2 O35297	O35297 mus musculus
5	1557	97.7	295	2 P97299	P97299 mus musculus
6	1550.5	97.3	294	2 Q863H1	Q863H1 canis famli
7	1515	95.0	283	2 Q9BG86	Q9BG86 oryctolagus
8	1318	82.7	295	2 Q6P8B8	Q6P8B8 xenopus tro
9	1299	81.5	292	2 Q9IA96	Q9IA96 gallus gall
10	1283	80.5	298	2 Q7XKM6	Q7XKM6 xenopus lae
11	1116	70.0	206	2 O14778	O14778 homo sapien
12	667.5	41.9	310	2 Q6TNR8	Q6TNR8 brachydanio
13	631	39.6	314	2 Q8K269	Q8K269 mus musculus
14	627	39.3	306	2 Q6GZK1	Q6GZK1 oryzias lat
15	627	39.3	314	2 Q9WU66	Q9WU66 mus musculus
16	619	38.8	315	2 Q9XSC1	Q9XSC1 bos taurus
17	618.5	38.8	296	2 Q7T2K9	Q7T2K9 brachydanio
18	618.5	38.8	315	2 Q640J3	Q640J3 xenopus lae
19	614.5	38.6	317	2 O14780	O14780 homo sapien
20	613.5	38.5	315	2 Q8AWG4	Q8AWG4 xenopus lae
21	611.5	38.4	315	2 Q6GL50	Q6GL50 xenopus tro
22	604	37.9	313	2 O00546	O00546 homo sapien
23	602	37.8	314	2 O14779	O14779 homo sapien
24	602	37.8	314	2 Q8N474	Q8N474 homo sapien
25	596.5	37.4	308	2 O19116	O19116 bos taurus
26	594	37.3	314	2 Q8R1J4	Q8R1J4 mus musculus
27	592	37.1	314	2 O08861	O08861 mus musculus
28	591.5	37.1	272	2 Q8C4U3	Q8C4U3 mus musculus
29	583.5	36.6	311	2 Q9YI24	Q9YI24 xenopus lae
30	573.5	36.0	314	2 Q9DEQ4	Q9DEQ4 gallus gall
31	501	31.4	307	2 O42397	O42397 gallus gall

RESULT 1

Q9HAP5 PRELIMINARY; PRT; 295 AA.

DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Pancreas tumor-related protein.

GN Name=FKSG12;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Wang Y.-G.;

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF311912; AAG24923.1; -

DR PIR; JE0174; JE0174.

DR HSSP; O61091; I1JY.

DR Genew; HGNC:10777; SFRP2.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO; GO:0007275; P:development; IEA.

DR InterPro; IPR000024; F2 domain.

DR InterPro; IPR001134; Netrin-C.

DR InterPro; IPR008993; TIMP_like.

DR Pfam; PF01392; Fz; 1.

DR Pfam; PF01759; NTR; 1.

DR SMART; SM00643; C345C; 1.

DR SMART; SM00063; FRI; 1.

DR PROSITE; PS0038; FZ; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

DR PROSITE; PS0189; NTR; 1.

QY 241 DLSQCTCEEMNDINAPYLVWGKQGGLVITSVKRWKQKQREFKRISSIRKLCQ 295
 DB 241 DLSQCTCEEMNDINAPYLVWGKQGGLVITSVKRWKQKQREFKRISSIRKLCQ 295

RESULT 2
 Q96HF1 PRELIMINARY; PRT; 295 AA.
 AC Q96HF1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Secreted frizzled-related protein 2 (SFRP-2).
 GN Name:SFRP2; ORFName:UNQ361;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; BC008666; AA08666.1; -;
 DR EMBL; AY359001; AA089360.1; -;
 DR HSSP; 061091; 1IJY.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR001134; Netrin C.
 DR InterPro; IPR008993; Timp-like.

DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF01759; NTR; 1.
 DR PROSITE; PS50038; Fz; 1.
 DR PROSITE; PS50189; NTR; 1.
 SQ SEQUENCE 295 AA; 33518 MW; 97597CFA541BF3D4 CRC64;

Query Match 99.7%; Score 1590; DB 2; Length 295;
 Best Local Similarity 99.7%; Pred. No. 1.2e-117;
 Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLOGPGLLLFLASHCCIGSARGLFLFGQPDFYFKRSNCKPPIANLQCHGIEYQNNRL 60
 DB 1 MLOGPGLLLFLASHCCIGSARGLFLFGQPDFYFKRSNCKPPIANLQCHGIEYQNNRL 60
 QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDPTKFLCSLFAPVCLDDLDDETIOPCHSLCVQ 120
 DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDPTKFLCSLFAPVCLDDLDDETIOPCHSLCVQ 120
 QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPASSDHLHPATEAPKVCACKKNND 180
 DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLCIPASSDHLHPATEAPKVCACKKNND 180
 QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTKIYKLVNGVSRDLKKSVLWLK 240
 DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTKIYKLVNGVSRDLKKSVLWLK 240
 QY 241 DLSQCTCEEMNDINAPYLVWGKQGGLVITSVKRWKQKQREFKRISSIRKLCQ 295
 DB 241 DLSQCTCEEMNDINAPYLVWGKQGGLVITSVKRWKQKQREFKRISSIRKLCQ 295

RESULT 3
 O08862 PRELIMINARY; PRT; 295 AA.
 AC O08862;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Secreted frizzled related protein SFRP-2 (Secreted frizzled-related
 sequence protein 2).
 GN Name:Sfrp2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97250455; PubMed=9096311; DOI=10.1073/pnas.94.7.2859;
 RA Ratner A., Hsieh J.C., Smallwood P.M., Gilbert D.J., Copeland N.G.,
 RA Jenkins N.A., Nathans J.;
 RT "A family of secreted proteins contains homology to the cysteine-rich
 ligand-binding domain of frizzled receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:2859-2863(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; BC008666; AA08666.1; -;
 DR EMBL; AY359001; AA089360.1; -;
 DR HSSP; 061091; 1IJY.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR001134; Netrin C.
 DR InterPro; IPR008993; Timp-like.


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RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017989; AAB70795.1; -.
DR HSSP; Q61091; 1IUY.
DR MGD; MGI:108078; Sfrp2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR008993; TIMP_Like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; Fz; 1.
DR PROSITE; PS50189; NTR; 1.
DR PROSITE; 295 AA; 33483 MW; 2D296C477C358762 CRC64;
SQ SEQUENCE

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Query Match	97.7%	Score 1557	DB 2	Length 295
Best Local Similarity	97.6%	Pred. No. 4.8e-115		
Matches 288	Conservative	3	Mismatches 4	Indels 0
				Gaps 0

QY	61	PNLLGHETNMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFAPVCLDDDLDETIPCHSLCQV	120
Db	61	PNLLGHETNMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFAPVCLDDDLDETIPCHSLCQV	120

Cy	KQRCATVMSAFGFPFDMLECDRF QDNDLCIPPLASSDHLLPALSEAPKYCEACKNND	180
121	KQRCATVMSAFGFPFDMLECDRF QDNDLCIPPLASSDHLLPALSEAPKYCEACKNND	180
D6	KQRCAPVMSAFGFPFDMLECDREFQDNDCIPLASSDHLLPATSEAPKYCEACKTKE	180

[illegible]

		DSLQTCCEEMNDINAPYLVGMQKGELVITSVKRWKQGREFKRISRSIRKLQC	295
Qy		DSLQTCCEEMNDINAPYLVGMQKGELVITSVKRWKQGREFKRISRSIRKLQC	295
		DSLQTCCEEMNDINAPYLVGMQKGELVITSVKRWKQGREFKRISRSIRKLQC	295
D _b		DSLQTCCEEMNDINAPYLVGMQKGELVITSVKRWKQGREFKRISRSIRKLQC	295

RESULT 5
P97299
TD P07206
PROB INTACTARY.
CCE
L
A

AC	P97299;
DT	01-MAY-1997 (TREMBlrel. 03, Created)
DD	01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DE SDF5 protein.
GN Name=Sfrp2; Synonyms=SDF5;
OS Mus musculus (Mouse).
ID 100000000

OC Buxaco, Oca, Metacoja, CnOdata; Vertebrata; Euteriostoma; OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090; [1]_ [1]

SEQUENCE FROM N.A.
RP MEDLINE=9702876; PubMed=8938438; DOI=10.1006/geno.1996.0560;
RX Shirozu M., Tada H., Tashiro K., Nakamura T., Lopez N.D., Nazarea M.,
RA Hamada T., Sato T., Nakano T., Honjo T.

RT "Characterization of novel secreted and membrane proteins insolated by
RT the signal sequence trap method."; GenomiCS 37:273-280.(1996).
RL EMRI: D50462..EAA03053.
DL

DR HSSP; Q61091; LIJY.
DR MGD; MG1:108078; Sfrp2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.

DR InterPro: IPR001134; Netrin C.
DR InterPro: IPR008993; TIMP_like.
DR Pfam: PF01392; Fz; 1.
DR

DR SMART; SMO0643; C345C; 1.
DR SMART; SMO0063; FRI; 1.

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DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 295 AA; 33501 MW; 2638770C77874C72 CRC64;

Query Match
Best Local Similarity 97.7%; Score 1557; DB 2; Length 295;
Matches 288; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLQPGSLLLLVASHCHCLGSARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
DB 1 MPRGPASLLLVASHCHCLGSARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120
QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLDCIPLASSDHLLPATEAPKVCACKNKND 180
DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLDCIPLASSDHLLPATEAPKVCACKNKND 180
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240
DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240
QY 241 DSLOQTCCEMNDINAPYLVMOQKQGGELVITSVKRWQKGQREFKRISRSIRKLQ 295
DB 241 DSLOQTCCEMNDINAPYLVMOQKQGGELVITSVKRWQKGQREFKRISRSIRKLQ 295

RESULT 6
ID Q863H1 PRELIMINARY; PRT; 294 AA.
AC Q863H1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Putative secreted frizzled related protein 2.
GN Name=sfrp2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=bred:Irish setter; TISSUE=Retina;
RA Lin C.T., Cocks J., Pierce-Kelling S., Squire M.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
[2]
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 294 AA; 33340 MW; 79C1FF3882CBE1B1 CRC64;

Query Match
Best Local Similarity 97.3%; Score 1550.5; DB 2; Length 294;
Matches 289; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 MLQPGSLLLLVASHCHCLGSARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
DB 1 MPRGPASLLLVASHCHCLGSARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
QY 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120
DB 61 PNLLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQ 120
QY 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLDCIPLASSDHLLPATEAPKVCACKNKND 180
DB 121 VKDRCAPVMSAFGFPWDMLECDRFPQNDLDCIPLASSDHLLPATEAPKVCACKNKND 180
QY 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240
DB 181 DDNDIMETLCKNDPALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLK 240
QY 241 DSLOQTCCEMNDINAPYLVMOQKQGGELVITSVKRWQKGQREFKRISRSIRKLQ 295
DB 241 DSLOQTCCEMNDINAPYLVMOQKQGGELVITSVKRWQKGQREFKRISRSIRKLQ 295

RESULT 7
ID Q9BG86 PRELIMINARY; PRT; 283 AA.
AC Q9BG86;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Secreted frizzled-related protein 2 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Levin J.M., Boubaker El Andaloussi R.A., Dainat J., Cabrolie M.,
RA Bacou F.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF323272; AAK11319.1; -.
DR HSSP; Q61091; 1IJY.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
FT NON TER 1
SQ SEQUENCE 283 AA; 32167 MW; CC75AD7F54D3D3ACB CRC64;

Query Match
Best Local Similarity 95.0%; Score 1515; DB 2; Length 283;
Matches 279; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 13 LASHCCCLGSARGFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNMLPNLLGHETMKEV 72
DB 1 LASHCCCLGSARGFLFGQPDFSHKRSNCKPIPATLQCHGIEYQNMLPNLLGHETMKEV 60
QY 73 LEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQVQRCAPVMSAF 132
DB 61 LEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDDETIQCHSLCVQVQRCAPVMSAF 120
QY 133 GFPMPDMLECDRFPQNDLDCIPLASSDHLLPATEAPKVCACKNKDDNDIMETLCKN 192
DB 121 GFPMPDMLECDRFPQNDLDCIPLASSDHLLPATEAPKVCACKNKDDNDIMETLCKN 180
QY 193 DFALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLKDSIQCTCEENND 252
DB 193 DFALKIKVKEITYINRDTKIILETKSTIYKLVNGVSRDLKKSVMWLKDSIQCTCEENND 252

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Qy	68	TMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAVCLDDLDDETIQPCHSLCVQVKDRCAP	127
Db	68	TMKEVQLQASSWIPLVQKQCHQDHTKKFLCSLFAVPCIDDLDETIKPCHSLCEQVKDSCAP	127
Qy	128	VNSAGFPWPDMECDRFPQNDLCIPLASSDHLLPATEAPKVCCEACKKNDDDDNDIME	187
Db	128	VNSAGFPWPDMECSRFPQNDLCIPASTHEVVPVTRAPKVCDCACKNSNEDNDIVE	187
Qy	188	TLCKNDFAKIKVKEITYINRDKIILLETSKTIYKLVGSERDLKKSVLWLKDSLQCTC	247
Db	188	NLCKNDFAKIKVKEIAYINGDKIIPETGKTIYKLVGTVTRDLKKTVLWLKDGLOCTC	247
Qy	248	EMNDINAPYLVMGQKQGGELVITSVKRWQKGQREPKRISRSIRKLQC	295
Db	248	DEMNDINAPYLVMGQKGGELVITSVKRWQKGQREPKRITRSIRKLQC	295
RESULT 9			
Q9IA96 PRELIMINARY; PRT; 292 AA.			
ID	Q9IA96		
AC	Q9IA96;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Secreted frizzled-related protein-2.		
GN	Name=Sfrp-2;		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=20123838; PubMed=10656762; DOI=10.1006/dbio.1999.9586;		
RA	Ladner R.K., Church V.L., Allen S., Robson L., Abdelfattah A.,		
RA	Brown N.A., Hattersley G., Rosen V., Luyten F.P., Dale L.,		
RA	Cloning and expression of the Wnt antagonists Sfrp-2 and Frzb during		
RT	chick development."		
RL	Dev. Biol. 218:183-198(2000).		
RL	EMBL; AF218056; AAF27642.1; -.		
DR	HSSP; Q61091; IUDY.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0004888; P:transmembrane receptor activity; IEA.		
DR	GO; GO:0007275; P:development; IEA.		
DR	InterPro; IPR000024; Fz_domain.		
DR	InterPro; IPR001134; Netrin C.		
DR	InterPro; IPR008993; TIMP_like.		
DR	Pfam; PF01392; Fz; 1.		
DR	Pfam; PF01759; NTR; 1.		
DR	SMART; SM00063; FRI; 1.		
DR	PROSITE; PS50038; Fz; 1.		
DR	PROSITE; PS50189; NTR; 1.		
SQ	SEQUENCE 292 AA; 33118 MW; 0490657229F475B1 CRC64;		
Query Match 81.5%; Score 1299; DB 2; Length 292;			
Best Local Similarity 81.1%; Pred. No. 1.2e-94;			
Matches 236; Conservative 20; Mismatches 35; Indels 0; Gaps 0;			
Qy	5	PGSLLLFLASHCCLGSGARGLFGPDFSYKRSNCKPIAPMLQLCHGIEYQNMRLPNLL	64
Db	2	PRRLCAULLLASQCLSGTAGLFFGPEPDFSYKESNCKPIAPMMLCRGIEYSMLPNLL	61
Qy	65	GHEWKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAVCLDDLDDETIQPCHSLCVQVKDR	124
Db	62	GHETVQVLEQATTWIPLVQKQCHPDTRKFLCSLFAVPCIDDLDETIQPCHSLCEVVKES	121
Qy	125	CAPVMSAFGFPWPDMECDRFPQNDLCIPLASSDHLLPATEAPKVCCEACKKNDDND	184
Db	122	CAPVMSAFGFPWPDMECDRFPQNDLCIPLASSDHILPVTREAPKVCDCACKKNEDND	181
Qy	185	IMETLCKNDFAKIKVKEITYINRDKIILLETSKTIYKLVGSERDLKKSVLWLKDSLQ	244

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Db 182 INENLCKNDPALKIKVKEIAYINGDTKITPFTKSTKIYKLNGLTERDLKIVLWLGGLQ 241
QY 245 CTCCEMNDINAPYLVWGQKQGGELVITSVKRWKQKQREPKRISIRKLQC 295
Db 242 CTCCEMNDINAPYLVWGQKQAGELVITSVKRWKQKQREPKRISIRKLQC 292

RESULT 10
Q7ZXMK PRELIMINARY; PRT; 298 AA.
AC Q7ZXMK;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sfrp2-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.K., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.;
RT Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044687; AAH44687.1; -.
DR HSSP; O61091; 1IJY.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF01392; Fz; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
FT NON TER 206
SQ SEQUENCE 298 AA; 33862 MW; D46857DAAC80DEB3 CRC64;

Db 182 INENLCKNDPALKIKVKEIAYINGDTKITPFTKSTKIYKLNGLTERDLKIVLWLGGLQ 241
QY 245 CTCCEMNDINAPYLVWGQKQGGELVITSVKRWKQKQREPKRISIRKLQC 295
Db 242 CTCCEMNDINAPYLVWGQKQAGELVITSVKRWKQKQREPKRISIRKLQC 292

RESULT 10
Q7ZXMK PRELIMINARY; PRT; 298 AA.
AC Q7ZXMK;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sfrp2-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.K., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.;
RT Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044687; AAH44687.1; -.
DR HSSP; O61091; 1IJY.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
FT NON TER 206
SQ SEQUENCE 298 AA; 33862 MW; D46857DAAC80DEB3 CRC64;

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Query Match 80.5%; Score 1283; DB 2; Length 298;
Best Local Similarity 80.9%; Pred. No. 2.3e-93;
Matches 233; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

QY 8 LLLFLASHCHCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRLPNLLGHE 67
Db 11 VVLVLLACDCMDSVRALFPFGQPEFSYKRSNCKPIPATVLCHEIEPNRLPNLLGHE 70

QY 68 TMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDLDLDETIOCHSLCVQVKRCAP 127
Db 71 SMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDLDLDETIOCHSLCVQVKRCAP 130

QY 128 VMSAFGFPWPDMLECDRFPQNDLICIPASSDHLPLATEAPKVCACKNDDNDIME 187
Db 131 VMSAFGFPWPDMLECDRFPQNDLICIPATNEHQVPTREAPKVCACKNDDNDIVE 190

QY 188 TLCKNDPALKIKVKEITVINRDTKIILETSKTIYKLNGLVSEKDLKSVLWLDLQCTC 247
Db 191 NLCKNDPALKIKVKEIAYINGDTKIIETKGTIYKLNGLVSEKDLKSVLWLDLQCTC 250

QY 248 EEMNDINAPYLVWGQKQGGELVITSVKRWKQKQREPKRISIRKLQC 295
Db 251 DEMNDINAPYLVWGQKQGGELVITSVKRWKQKQKFKRITRSIRKLQC 298

RESULT 11
O14778 PRELIMINARY; PRT; 206 AA.
ID O14778;
AC O14778;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Secreted apoptosis related protein 1 (Fragment).
GN Name=GARPI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98054286; PubMed=9391078; DOI=10.1073/pnas.94.25.13636;
RA Melkonian H.S., Chang W.C., Shapiro J.P., Mahadevappa M.,
RA Fitzpatrick P.A., Kiefer M.C., Tomei L.D., Umansky S.R.;
RT "SARPs: a family of secreted apoptosis-related proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:13636-13641(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Melkonian H., Prochazka V., Umansky S.R.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017986; AAB70792.1; -.
DR HSSP; O61091; 1IJY.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF01392; Fz; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
FT NON TER 206
SQ SEQUENCE 206 AA; 23215 MW; 126A434B9EBE62845 CRC64;

Query Match 70.0%; Score 1116; DB 2; Length 206;
Best Local Similarity 98.6%; Pred. No. 2.4e-80;
Matches 205; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 MLQPGSLLILFLASHCHCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60
Db 1 MLQPGSLLILFLASHCHCLGSARGLFLFGQPDFSYKRSNCKPIPANLQCHGIEYQNRL 60

QY 61 PNLLGHETMKVEVLQAGAWIPLVMKQCHPDTKKFLCSLFAFVCLDLDLDETIOCHSLCVQ 120

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Db 61 PNLGHETMKEVLEQAGAWIPLVMKQCHPDTKFLCSLPAPVCLDLDLDTIQCHSRVQ 120
Qy 121 VKDRCAPVNSAFGPPWDMLECDRFPQDNDLCIPLASSDHLHPATEEAPKVCACKNKD 180
Db 121 VKDRCAPVNSA--FPWDMLECDRFPQDNDLCIPLASSDHLHPATEEAPKVCACKNKD 178
Qy 181 DNDIMETLCKNDFALKIKVKEITYINR 208
Db 179 DNDIMETLCKNDFALKIKVKEITYINR 206

RESULT 12
Q6YNR8 PRELIMINARY; PRT; 310 AA.
AC Q6YNR8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Secreted frizzled-related protein 1.
GN Name=frp1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin J., Kim S.H., Yoo S.Y., Huh T.L.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY050560; AAL11439.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR PROSITE; PS50038; FRI; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 310 AA; 35393 MW; 77D3412C6CC8EA4 CRC64;

Query Match 41.9%; Score 667.5; DB 2; Length 310;
Best Local Similarity 47.2%; Pred. No. 1.1e-44;
Matches 125; Conservative 51; Mismatches 80; Indels 9; Gaps 5;

Qy 33 FSYKRSNCKPIPANLQCHGIEYQNNRLPNLGHETMKEVLEQAGAWIPLVMKQCHPDTK 92
Db 45 FYAKQPCVDIIPADLRLCYNVGVKWRPNLLDHTMPEVKQAGSWPLAKRCHADTQ 104
Qy 93 KFLCSLPAPVCLDLDLDTIQCHSLCVQKRCAPVNSAFGPPWDMLECDRFPQDNDLC 152
Db 105 VFLCSLPAPVC---LDRPIYPCRSLEAVRDSAPVMETGPPWPEMLQCEKFPIDNLC 161
Qy 153 IPLA--SSDHLHPATE--EAPKVCACKNKDNDNDIMETLCKNDFALKIKVKEITYINRDT 210
Db 162 IPMQFSAGH---ATQTPVSKVPCPDNELKADT--IMHYCASDFALKIKVKEIKEGDR 217
Qy 211 KIILETKSTIYKLVGVSERDLKSVLWLDKSLQCTCEMNDINAPYLVMGQKQGGELVI 270
Db 218 KLIAAQKKVLLKGLRKDLKLLTYIKNGANCPSCQLDNLGNSFLIMGRKVDQQLL 277
Qy 271 TSVKRWQKGQREFKRSIRSLKQC 295
Db 278 MSIHKWDKSKELKPAIKYSQOC 302

RESULT 13
Q8K269 PRELIMINARY; PRT; 314 AA.
ID Q8K269
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AC Q8K269;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Secreted frizzled-related sequence protein 5.
GN Name=Strps;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaltus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032921; AAM32921.1; -.
DR HSSP; Q61091; IJY.
DR MGD; MGI:1860298; Sfrp5.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR PROSITE; PS50038; FRI; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 314 AA; 35409 MW; 29775FF26513B7DA CRC64;

Query Match 39.6%; Score 631; DB 2; Length 314;
Best Local Similarity 44.2%; Pred. No. 9e-42;
Matches 125; Conservative 49; Mismatches 83; Indels 26; Gaps 7;

Qy 19 LGSARGLFLFGQPDFSY-----KRSNCKPIPANLQCHGIEYQNNRLPNLL 64
Db 16 LGALHGAPTRGQ--EYDYGWQAEPHGRSYSKPPQCLDIPADLPLCHTVGYKRMRLPNLL 74
Qy 65 GHETMKEVLEQAGAWIPLVMKQCHPDTKFLCSLPAPVCLDLDLDTIQCHSLCVQKDR 124
Db 75 EHESLAEVQQAQSWPLAKRCHSDTQVFLCSLPAPVC---LDRPIYPCRSLEAVRAG 131
Qy 125 CAPVNSAFGPPWDMLECDRFPQDNDLCIPLASSDHLHPATEEAP---KVCACKNKD 181
Db 132 CAPLMEAYGFPWPEMLCHKFPDNDLCIAVQFGH--LPAT--APPYTKIQAQCEMEHSA 187
Qy 182 DNDIMETLCKNDFALKIKVKEITYINRDTKIILETKSTIYKLVGVSERDLKSVLWLDK 241
Db 188 DG--LMEQWCSSDFVVKMRIKEIKIDNGDRKLIQAQKKKLLKAGPLKRRKDTKVLHMK 246
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QY 242 SLQCTCEEMNDINAPYLVMGKQGGLVITSVKRWKQKQREFK 284
Db 247 GASCPQDNLNLTGSLVNGKRVGQQLLTAVYRWDKKNKEMK 289

RESULT 14
Q6GZK1
ID Q6GZK1 PRELIMINARY; PRT; 306 AA.
AC Q6GZK1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Secreted frizzled-related protein 1.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15210177; DOI=10.1016/j.mod.2004.03.003;
RA Esteve P., Lopez-Rios(1) J., Bovolenta P.;
RT "SRP1 is required for the proper establishment of the eye field in
RT the medaka fish.";
RL Mech. Dev. 121:687-701 (2004).
DR EMBL; AY560904; AAS59408.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS0038; FZ; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 306 AA; 34955 MW; 6D49B0FB9682C48C CRC64;

Query Match 39.3%; Score 627; DB 2; Length 306;
Best Local Similarity 39.9%; Pred. No. 1.8e-41;
Matches 123; Conservative 54; Mismatches 87; Indels 44; Gaps 9;

QY 9 LLLFLASHCCLGSLGFLFGQPDFSY-----KRSNCKPIPANLQCHGIE 54
Db 14 LVLLAVTC-----GASEYEYTWAGSYNGRGYKAPQCVDPDDLRLCHTVG 62

QY 55 YQNMRLPNLLGHETWKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDLDTIQPC 114
Db 63 YQMLLPNLLHETWAEVKQQAASSWVPLVHKNCHKDTQVFLCALFAPVC---MERPIYPC 119

QY 115 HSLCVQVKDRCAPVSAFGFPMDLDCDRFPQDNDLCIPLASSDHLLPATEEA-----P 169
Db 120 RWLCETVRDSCSPIMEAFGFPPEMLTCDKFPQDG-VCIAVTQPN----ATEATWPSGHS 174

QY 170 KVCEACKN--KNDDNDIMETLCKNDFAKIKVKEITYINRDTKIILETKSKTIYKLVNGV 227
Db 175 PACPPCDNEIKND---AMLENICASEFALKAKIKEVKQENMDRKVILQ-RRKRMVKQGNL 230

QY 228 SERDLKKSVLWIKDSLOCTCEEMNDINAPYLVMGKQGGLVITSVKRWKQKQREFK 287
Db 231 KKRDLLKLTLYLKGANCPCQQLLENQYLIMGRKVDKQFLLTGTHKWDKSKFEKKIM 290

QY 288 RSIRKLQ 295
Db 291 KKLKNYKC 298
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RESULT 15
Q9WU66

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ID Q9WU66 PRELIMINARY; PRT; 314 AA.
AC Q9WU66;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Secreted frizzled-related protein 5.
GN Name=Sfrp5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang J.T., Esumi N., Moore K., Li Y., Zhang S., Chew C., Goodman B.,
RA Rattner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
RT "Cloning and characterization of a secreted frizzled-related protein
RT that is expressed by the retinal pigment epithelium.";
RL Hum. Mol. Genet. 0:0-0 (1999).
DR EMBL; AF117759; AAD25053.1; -.
DR HSP; Q61091; I1JY.
DR MGD; MGI:1860298; Sfrp5.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS0038; FZ; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 314 AA; 35381 MW; 296847F56D1CAFDD CRC64;

Query Match 39.3%; Score 627; DB 2; Length 314;
Best Local Similarity 43.8%; Pred. No. 1.9e-41;
Matches 124; Conservative 49; Mismatches 84; Indels 26; Gaps 7;

QY 19 LGSARGLFLFGQPDFSY-----KRSNCKPIPANLQCHGIEYQNMRLPNLL 64
Db 16 LGALHGAPTRGQ-EYDYGWQAEPLHGRSYSKPPQCLDIPADLPFLCHTVGYKRMRLPNLL 74

QY 65 GHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLPAPVCLDDLDLDTIQCHSLCVQVKDR 124
Db 75 EHESLAEVKQAASSWLPPLAKRCHSDTQVFLCSLPAPVC---LDRPIYPCSLCEAARAG 131

QY 125 CAPVMSAFGFPMDLDCDRFPQDNDLCIPLASSDHLLPATEAP---KVCEACKNKND 181
Db 132 CAPLMEAYGFPWPEMLHCHKPFLDNLDCIAVQFGH--LPAT--APPVTKICAQCEMEHSA 187

QY 182 DNDIMETLCKNDFAKIKVKEITYINRDTKIILETKSKTIYKLVNGVSRDLKKSVLWIKD 241
Db 188 DG-LMEQWCSDFVYVKRIKEIKIDNGDRKLIGAKKKKLLKAGPLKKRDKTKLVLMKN 246

QY 242 SLQCTCEEMNDINAPYLVMGKQGGLVITSVKRWKQKQREFK 284
Db 247 GASCPQDNLNLTGSLVNGKRVGQQLLTAVYRWDKKNKEMK 289

Search completed: September 1, 2005, 10:54:24
Job time : 122.518 secs
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GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 1, 2005, 09:26:23 ; Search time 315.5 Seconds
(without alignments)
6579.934 Million cell updates/sec

Title: US-08-949-904A-1
Perfect score: 3585
Sequence: 1 GAATTCGGCCTTCATGGCT.....AAAAAAGGCGCGCGC 2027

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+ n2p model -DEV=xlp
-Q/cgn2_1/USFTO_spool_P/US08949904/runat_01092005_102612_21247/app.query.fasta_1.2183
-DB=uniprot -QFMT=fasta -SUFFIX=rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptb -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08949904 @CEN 1.1 401 @runat_01092005_102612_21247 -NGBU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1594	44.5	295	Q9HAP5	Q9hap5 homo sapien
2	1590	44.4	295	Q96HF1	Q96hf1 homo sapien
3	1560	43.5	295	O08862	O08862 mus musculus
4	1557	43.4	295	O35297	O35297 mus musculus
5	1557	43.4	295	P97299	P97299 mus musculus
6	1550.5	43.2	294	O863H1	O863h1 canis famil
7	1515	42.3	283	O29B86	O29b86 oryctolagus
8	1318	36.8	295	O6F8B8	O6f8b8 xenopus tro
9	1299	35.8	292	O7A9E6	O7a9e6 gallus gall
10	1283	35.8	298	O72XM6	O72xm6 xenopus lae
11	1116	31.1	206	O14778	O14778 homo sapien
12	670.5	18.7	310	O6VNR8	O6vnr8 brachydanio
13	641	17.9	314	O8X269	O8x269 mus musculus
14	637	17.8	314	O9WU66	O9wu66 mus musculus
15	629	17.5	315	O9XSC1	O9xsc1 bos taurus
16	627	17.5	306	O6GZK1	O6gzk1 oryzias lat

17	624	17.4	317	2	O14780	O14780 homo sapien
18	618.5	17.3	296	2	Q7T2K9	Q7t2k9 brachydanio
19	618.5	17.3	315	2	O640J3	O640j3 xenopus lae
20	613.5	17.1	315	2	Q8AWG4	Q8awg4 xenopus lae
21	611.5	17.1	315	2	Q6GLS0	Q6gl50 xenopus tro
22	608	17.0	313	2	O00546	O00546 homo sapien
23	606.5	16.9	314	2	O14779	O14779 homo sapien
24	606.5	16.9	314	2	Q8N474	Q8n474 homo sapien
25	603.5	16.8	308	2	O19116	O19116 bos taurus
26	597	16.7	314	2	Q8RLJ4	Q8rlj4 mus musculus
27	595	16.6	314	2	O08861	O08861 mus musculus
28	591.5	16.5	272	2	Q8C4U3	Q8c4u3 mus musculus
29	583.5	16.3	311	2	Q9Y124	Q9y124 xenopus lae
30	575.5	16.1	314	2	Q9DEQ4	Q9deq4 gallus gall
31	503.5	14.0	307	2	O42397	O42397 gallus gall
32	498	13.9	295	2	Q91897	Q91897 xenopus lae
33	484.5	13.5	300	2	Q8F2E8	Q8f2e8 xenopus tro
34	483	13.5	282	2	Q8JHC7	Q8jhc7 brachydanio
35	468	13.1	121	2	Q919F4	Q919f4 xenopus lae
36	433.5	12.1	280	2	Q91AUS	Q91aus xenopus lae
37	431.5	12.0	284	2	Q90ZA6	Q90za6 ambystoma m
38	422.5	11.8	281	2	Q73821	Q73821 xenopus lae
39	413.5	11.5	282	2	Q7SX78	Q7sx78 brachydanio
40	399	11.1	77	2	Q80W55	Q80w55 rattus norv
41	380.5	10.6	260	2	Q9GUF5	Q9gu55 caenorhabdi
42	351.5	9.8	115	2	Q90ZG8	Q90zg8 brachydanio
43	319	8.9	750	2	O810L8	O810l8 mus musculus
44	314	8.8	158	2	Q9R168	Q9r168 rattus norv
45	303.5	8.5	642	2	Q7TS82	Q7ts82 mus musculus

ALIGNMENTS

RESULT 1

Q9HAP5 PRELIMINARY; PRT; 295 AA.
ID Q9HAP5;
AC Q9HAP5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Pancreas tumor-related protein.
GN Name=FKSG12;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang Y.-G.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF311912; -AAG24923.1;
DR PIR; JF0174; JE0174.
DR HSP; G61091; IJY.
DR Gnew; HGNC:10777; SFRP2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin C.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 295 AA; 33490 MW; 97597971541BFC4 CRC64;
Alignment Scores: 2.16e-90 Length: 295
Pred. No.: 1594.00 Matches: 295
Score: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0


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Query Match: 44.46% Indels: 0
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QY 256 ATGCTCAGGGCCCTCGCTCGCTGCTGCTCTTCTTCCTCGCTCGCTCGCTCGCTCGGCG 315
DB |||||||
DB 1 MetLeuGlnGlyProGlySerLeuLeuLeuLeuPheLeuAlaSerHisCysLeuGly 20
QY 316 TCGGCGCGGGCTCTCTCTTTTGGCCAGCCCGACTTCTCTCTACAGCGCAATATGCG 375
DB |||||||
DB 21 SerAlaArgGlyLeuPheLeuPheGlyGlnProAspPheSerTyrLysArgSerAsnCys 40
QY 376 AGCCCATCCCGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
DB |||||||
DB 41 LysProIleProAlaAsnLeuGlnLeuCysHisGlyLeuGluTyrGlnAsnMetArgLeu 60
QY 436 CCCAACTCTGCTGGCCAGCAGACCATGAAGAGGTGCTGGAGCAGCGCGCTTGGATC 495
DB |||||||
DB 61 ProAsnLeuGlyHisGluThrMetLysGluValLeuGluGluAlaGlyAlaIle 80
QY 496 CCGTGTGTCATGAAGCAGTGCACCGGACACCAAGATTCTCTGCTGCTGCTCTTCGCC 555
DB |||||||
DB 81 ProLeuValMetLysGlnCysHisProAspThrLysLysPheLeuCysSerLeuPheAla 100
QY 556 CCGCTGCTGCTGATGACCTAGACGACGACGACCATCCAGCCATGCTGCTGCTGCTGCTG 615
DB |||||||
DB 101 ProValCysLeuAspLeuAspGluThrIleGlnProCysHisSerLeuCysValGln 120
QY 616 GTGAGGACCGCTGGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
DB |||||||
DB 121 ValLysAspArgCysAlaProValMetSerAlaPheGlyPheProTyrProAspMetLeu 140
QY 676 GAGTGGACCGCTTTCCCGGACCAACGACCTTTGTCATCCCCCTCGCTAGCAGCACCAC 735
DB |||||||
DB 141 GluCysAspArgPheProGlnAspAsnAspLeuCysIleProLeuAlaSerSerAspHis 160
QY 736 CTCTGCGCAGCAGCAGCAAGCTCAAGAGTATGTGAAGCTCGAATAAATAAATGAT 795
DB |||||||
DB 161 LeuLeuProAlaThrGluGluAlaProLysValCysGluAlaCysLysAsnLysAsnAsp 180
QY 796 GATGACAACGACATATGAACGCTTTGTAATAATGATTTTCTGCTGCTGCTGCTGCTGCT 855
DB |||||||
DB 181 AspAspAsnAspIleMetGluThrLeuCysLysAsnAspPheAlaLeuLysIleLysVal 200
QY 856 AAGGAGATAACCTACATCAACCGAGATACCAAAATCATCTCTGGAGACCAAGCAAGACC 915
DB |||||||
DB 201 LysGluIleThrTyrIleAsnArgAspThrLysIleIleLeuGluThrLysSerLysThr 220
QY 916 ATTTACAGCTGAACGGTGTGTCGGAAGGACCTGAAGAAATCGGTGCTGTGGCTCAAA 975
DB |||||||
DB 221 IleTyrLysLeuAsnGlyValSerGluArgAspLeuLysLysSerValLeuTrpLeuLys 240
QY 976 GACAGCTTCAGTGCACCTGTCAGAGATGAACGACATCAACGCGCCCTATCTGCTCATG 1035
DB |||||||
DB 241 AspSerLeuGlnCysThrCysGluGluMetAsnAspIleAsnAlaProTyrLysValMet 260
QY 1036 GGACAGAAACAGGGTGGGAGCTGTGTGATCACCTCGTGAAGCGGTGGCAGAGGGCGAG 1095
DB |||||||
DB 261 GlyGlnLysGlnGlyGluLeuValIleThrSerValLysArgTyrGlnLysGlyGln 280
QY 1096 AGAGAGTTCAACGGATCTCCCGGACGATCCCGAAGCTGCGATGC 1140
DB |||||||
DB 281 ArgGluPheLysArgIleSerArgSerIleArgLysLeuGlnCys 295
RESULT 2
Q96HF1
ID Q96HF1 PRELIMINARY; PRT; 295 AA.
AC Q96HF1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Secreted frizzled-related protein 2 (SFRP-2).
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GN Name=SPRP2; ORFNames=UNQ361;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; BC008666; AAH08666.1; -.
DR EMBL; AY359001; AAQ89360.1; -.
DR HSSP; Q61091; 1IJY.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR008993; TIMP-like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 295 AA; 33518 MW; 97597CFA541BF3D4 CRC64;
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Alignment Scores:
Pred. No.: 3,83e-90 Length: 295
Score: 1590.00 Matches: 294
Percent Similarity: 99.66% Conservative: 0
Best Local Similarity: 99.66% Mismatches: 1
Query Match: 44.35% Indels: 0
DB: 2 Gaps: 0
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Db      168 AlaProLysValCysAspLysValSerAsnGluAspAsnAspLysValGlu 187
QY      817 AGCTTTGTAATAATGTTTGCACGTAATAAAGTGAAGAGATAACCTACATCAAC 876
Db      188 AsnLeuCysLysAsnAspPheAlaLeuLysLysValLysGluLysLysValLysLeu 207
QY      877 CGAGATACCAAAATCATCTGGAGACCAAGACAGACCAATTCACAGCTGAACGGTGTG 936
Db      208 GlyAspThrLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 227
QY      937 TCCGAAAGGAGCCTGAAGAAATCGGTGCTGCTCAAAAGACAGCTTGAGTGCACCTGT 996
Db      228 ThrGluArgAspLeuLysLysLysLysLysLysLysLysLysLysLysLys 247
QY      997 GAGGAGATGAACACATCAACCGCGCTTCTGTCATCGGACAGAAACAGGCTGGGAG 1056
Db      248 AspGluMetAsnAspLysLysLysLysLysLysLysLysLysLysLysLys 267
QY      1057 CTGCTGATCACTCGGTGAAGCGTGGCAGAGGGGCGAGAGAGTTCAAGCGCATCTCC 1116
Db      268 LeuValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 287
QY      1117 CGCAGCATCCGCAAGCTGCAGTGC 1140
Db      288 ArgSerLysArgLysLeuGlnCys 295

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RESULT 9

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Q9IA96 PRELIMINARY; PRT; 292 AA.
AC Q9IA96;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Secreted frizzled-related protein-2.
GN Name=Sfrp-2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2023838; PubMed=10656762; DOI=10.1006/dbio.1999.9586;
RA Lader R.K., Church V.L., Allen S., Robson L., Abdelfattah A.,
RA Brown N.A., Hattersley G., Rosen V., Luyten F.P., Dale L.,
RA Francis-West P.H.;
RT "Cloning and expression of the Wnt antagonists Sfrp-2 and Frzb during
RT chick development.";
RL Dev. Biol. 218:183-198(2000).
DR EMBL; AF218056; AAF27642.1; -.
DR HSSP; Q61091; 1IDJ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR001334; Netrin.C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 292 AA; 33118 MW; 0490657229F475B1 CRC64;

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Alignment Scores:

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Pred. No.: 3,87e-72 Length: 292
Score: 1299.00 Matches: 236
Percent Similarity: 87.9% Conservative: 20
Best Local Similarity: 81.10% Mismatches: 35
Query Match: 36.23% Indels: 0
DB: 2 Gaps: 0

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US-08-949-904A-1 (1-2027) x Q9IA96 (1-292)
QY      268 CTGCTCGCTGCTGCTGCTCTCTCTCGCTCGCACTGCTGCTGGGCTCGCGCGCGGG 327
Db      2 ProArgArgLeuCysAlaLeuLeuLeuAlaSerGlnCysLeuGlySerThrAlaGly 21
QY      328 CTCCTCTCTTTGGCCAGCCGAGCTTCTCTACAGCGCAGCAATTTCAAGCCCATCCG 387
Db      22 LeuPheProPheGlyGluProAspPheSerTyrLysArgSerAsnCysLysProlePro 41
QY      388 GCCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 447
Db      42 AlaProMetLeuLeuCysArgGlyLysLysLysLysLysLysLysLysLysLys 61
QY      448 GGCCACGAGACATGAAGAGGTGCTGAGCAGCGCGCTTGGATCCCTGCTGCTGCTGCT 507
Db      62 GlyHisGluThrValGlnGluValLeuGluGlnAlaThrThrTrpLysProLeuValGln 81
QY      508 AAGCAGTGCACCCGACACCAAGAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 567
Db      82 LysGlnCysHisProAspThrArgLysPheLeuCysSerLeuPheAlaProValCysLys 101
QY      568 GATGACCTAGACGAGACCATCCAGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 627
Db      102 AspAspLeuAspGluLysLysLysLysLysLysLysLysLysLysLysLysLys 121
QY      628 TGCGCCCGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 687
Db      122 CysAlaProValMetSerAlaPheGlyPheProTrpProAspMetLeuAspCysSerArg 141
QY      688 TTCCCGCAGGACACGACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 747
Db      142 PheProLysAspAsnAspLeuCysLysLysLysLysLysLysLysLysLysLysLys 161
QY      748 ACCGAGGAAGCTCCAAAGGTATGTGAAGCTGCAAAATATAAAATATGATGATGATG 807
Db      162 ThrArgGluAlaProLysValCysAspAlaCysLysAsnLysAsnGluAspAsnAsp 181
QY      808 ATAATGGAACGCTTTGTAAATATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867
Db      182 IleMetGluAsnLeuLysLysAsnAspPheAlaLeuLysLysLysLysLysLysLys 201
QY      868 TACATCAACCGAGATACCAAAATCATCTGAGACCAAGACCAAGACCAATTTCAAGCTG 927
Db      202 TyrIleAsnGlyAspThrLysLysLysLysLysLysLysLysLysLysLysLysLys 221
QY      928 AACGGTGTGTCGAAAGGGACCTGAAGAAATCGGTGCTGCTGCTGCTGCTGCTGCTG 987
Db      222 AsnGlyLeuThrGluArgAspLeuArgLysLysLysLysLysLysLysLysLysLys 241
QY      988 TGCACCTGTGAGGAGATGAACGACATCAACCGCGCTTATCTGCTCATGGGACAGAAACAG 1047
Db      242 CysThrCysAspGluMetAsnAspLysLysLysLysLysLysLysLysLysLysLys 261
QY      1048 GGTGGGAGCTGTGATCACCTCGGTGAAGGGTGGCAGAGGGGCGACAGAGAGTTCAAG 1107
Db      262 AlaGlyGluLeuValLysLysLysLysLysLysLysLysLysLysLysLysLys 281
QY      1108 CGCATCTCTCCGACGATCCCGCAAGCTGCAGTGC 1140
Db      282 ArgPheSerArgSerLysLysLysLysLysLysLysLysLysLysLysLysLys 292
RESULT 10
Q7ZXM6 PRELIMINARY; PRT; 298 AA.
AC Q7ZXM6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sfrp2-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

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QY 1002 GATGAACGACATCAACGCCGCTTATCTGGTCATGGACAGAAACAGGGTGGGAGCTGCT 1061
Db 254 nleuAspAsnLeuThrGlySerPheLeuValMetGlyArgLysValGluGlyGlnLeuLe 274
QY 1062 GATCACCCTCGGTGAACGGCTGGCAGAAAGGGCGGAGAGAGATTCAAG 1107
Db 274 uleuThrAlaValTyArgTrpAspLysLysAsnLysGluMetLys 289

RESULT 14
Q9WU66 PRELIMINARY; PRT; 314 AA.
AC Q9WU66;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-OCT-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Secreted frizzled-related protein 5.
GN Name=Sfrp5;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang J.T., Esumi N., Moore K., Li Y., Zhang S., Chew C., Goodman B.,
RA Ratner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
RT "Cloning and characterization of a secreted frizzled-related protein
RT that is expressed by the retinal pigment epithelium.";
RL Hum. Mol. Genet. 0:0-0(1999).
DR EMBL; AF117759; AAD25053.1; -.
DR HSSP; Q61091; 11JY.
DR MGD; MGI:1860298; Sfrp5.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR SMART; SM00063; FRI; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 314 AA; 35381 MW; 296847P56D1CAPDD CRC64;

Alignment Scores:
Pred. No.: 3.58e-31 Length: 314
Score: 637.00 Matches: 132
Percent Similarity: 58.23% Conservative: 52
Best Local Similarity: 41.77% Mismatches: 91
Query Match: 17.77% Indels: 41
DB: 2 Gaps: 7

US-08-949-904A-1 (1-2027) x Q9WU66 (1-314)
QY 186 GCTCGAAGTCGCGCGCTCGCCCTTCCCGGCTCGCTCCCTCGCCCGCTCGGGTGC 245
Db 7 AlaArgThrAlaAlaLeuAlaLeuLeuGlyAlaLeuHisGlyAlaProThrArgGly 26
QY 246 CGCGCCCGACGATGCTGCAGGGGCCCTGGCTCGTGTGCTCTCTCCCTCGCCCTCGCACTG 305
Db 27 GlnGluTyAspTyTyGly----- 33
QY 306 CTGCTGGGCTCGCGCGGGCTCTTCTCTTGGCCAGCCGCTCTCTCTCAAGGG 365
Db 34 -----TrpGlnAlaGluProLeu-HisGlyAr 42
QY 366 CAGCAATTGCAAGCCC-----ATCCCGGCCAACCTGCAGCTGTGCCACGG 410
Db 42 gSerTySerLysProProGlnCysLeuAspLeuProAlaAspLeuProLeuCysHisTh 62
QY 411 CATCAATACCAAGACATCGCGCTCCCAACTGCTGGGCCACGAGACCATGAAGAGGT 470
Db 62 rValGlyTyLysArgMetArgLeuProAsnLeuLeuGluHisGluSerLeuAlaGluVa 82

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QY 471 GCTGGAGCAGCGCCGGCGCTTCGATCCCGCTCGTCTATGAGCAGTCCGACCGGACACCAA 530
Db 82 llyeGlnGlnAlaSerSerTrpLeuProLeuLeuAlaLysArgCysHisSerAspThrG1 102
QY 531 GAAGTTCTGCTGCTCGCTTTCGCGCCCGCTGCTGCTCGATGACCTAGACGAGACCATCCA 590
Db 102 nValPheLeuCysSerLeuPheAlaProValCys-----LeuAspArgProIleTy 119
QY 591 GCCATGCCACTCGCTCTGCTGAGGAGGAGGAGCGCTGCGCCCGCTCATGTCGCGCTT 650
Db 119 rProCysArgSerLeuCysGluAlaAlaArgAlaGlyCysAlaProLeuMetGluAlaTy 139
QY 651 CGGCTTCCCTGGCCCGACATGCTTGAGTGCAGCGTTTCCCGGACGACAGACCTTTG 710
Db 139 rGlyPheProTrpProGluMetLeuHisCysHisLysPheProLeuAsnAspLeuCy 159
QY 711 CATCCCCCTCGCTAGCAGCACCCTCTCTCCAGCAGCGGAGGAGGAGCTCCA----- 762
Db 159 sileAlaValGlnPheGlyHis-----LeuProAlaThr-----AlaProProValTh 175
QY 763 -AAGGTATGTGAAGCTGCAAAAATAAATAATGATGATGACGACCAACGACATAATGGAAACGCT 821
Db 175 rLysileCysAlaGlnCysGluMetGluHisSerAlaAspGly--LeuMetGluGlnMe 194
QY 822 TTGTAATAATGATTTGCACTGAAATAAAGTGAAGAGATACCTACATCAACCCGAGA 881
Db 194 tCysSerSerAspPheValValLysMetArgileGlyleLysileAspAsnGlyAs 214
QY 882 TACCAAAATCATCTGGAGACCAAGAGCAACGACATTTACAAAGCTGAACGGTGTGTCCGA 941
Db 214 pArgLysleuileGlyAlaGlnLysLysLysLysLysLysLysAlaGlyProLeuLysAr 234
QY 942 AAGGACCTGAAGAAATCGTGTGCTGCTCAAAAGACAGCTTGCAGTGCACCTGTGAGA 1001
Db 234 gLysAspThrLysLysLeuValLeuHisMetLysAsnGlyAlaSerCysProCysProG1 254
QY 1002 GATGAACGACATCAACGCCGCTTATCTGGTCATGGACAGAAACAGGGTGGGAGCTGCT 1061
Db 254 nLeuAspAsnLeuThrGlySerPheLeuValMetGlyArgLysValGluGlyGlnLeuLe 274
QY 1062 GATCACCCTCGGTGAACGGCTGGCAGAAAGGGCGGAGAGAGATTCAAG 1107
Db 274 uleuThrAlaValTyArgTrpAspLysLysAsnLysGluMetLys 289

RESULT 15
Q9XSC1 PRELIMINARY; PRT; 315 AA.
AC Q9XSC1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Secreted frizzled-related protein 5.
GN Name=sfrp5;
OS Bos taurus (Bovine);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang J.T., Esumi N., Moore K., Li Y., Zhang S., Chew C., Goodman B.,
RA Ratner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
RT "Cloning and characterization of a secreted frizzled-related protein
RT that is expressed by the retinal pigment epithelium.";
RL Hum. Mol. Genet. 0:0-0(1999).
DR EMBL; AF117757; AAD25051.1; -.
DR HSSP; Q61091; 11JY.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR001134; Netrin_C.

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DR InterPro: IPR008993; TIMP_like.

DR Pfam: PF01392; Fz; 1.

DR Pfam: PF01759; NTR; 1.

DR SMART: SM00643; C345C; 1.

DR SMART: SM00063; FRI; 1.

DR PROSITE: PS0038; FZ; 1.

DR PROSITE: PS0189; NTR; 1.

SQ SEQUENCE 315 AA; 35279 MW; 8B6E94951060A976 CRC64;

Alignment Scores:

Pred. No.:	1,12e-30	Length:	315
Score:	629.00	Matches:	132
Percent Similarity:	57.14%	Conservative:	52
Best Local Similarity:	40.99%	Mismatches:	97
Query Match:	17.55%	Indels:	41
DB:	2	Gaps:	7

US-08-949-904A-1 (1-2027) x Q9XSC1 (1-315)

QY	168	AGAGCGGCGCGGACCAAGCTCGAACTCCGGCGCGCTCGCCCTTCCCGGCTCCGCTCCC	227
Db	2	ArgAlaAlaAlaGlyGlyAlaArgAlaAlaValLeuAlaLeuLeuGlyAlaLeuHis	21
QY	228	TCTGCCCTCCGGGTCGGCGCCACAGATGTCGAGGCGCTCGCTCGCTGCTGCT	287
Db	22	GlyAlaProAlaArgGlyGluGluTyrAspTyrTyrGly-----	34
QY	288	CTTCTCTCGCTCGCACTGCTGCTGGCTCGGCGCGGCTCTTCTCTTTGGCCAGCC	347
Db	35	-----trp-GlnTh	37
QY	348	CGACTTCTCTACAGCGGACGAATTCGAAGCCC-----ATCCCGGCCAA	392
Db	37	rGluProLeuHisGlyArgSerTyrSerLysProGlnCysLeuAspIleProAlaAs	57
QY	393	CTGTGAGCTGTGCCAGGATCGAATACCAAGACATCGCGCTGCCAACCTGCTGGGCCA	452
Db	57	pleuProLeuCysHisThrValGlyTyrLysArgMetArgLeuProAsnLeuLeuGluHi	77
QY	453	CGAGACCATGAAGAGTCTGTGAGCAGCGCGCTTGGATCCGCTGTCATGAAGCA	512
Db	77	sGluSerLeuAlaGluValLysGlnGlnAlaSerSerTrpLeuProLeuLeuAlaLysAr	97
QY	513	GTGCCACCCGGACACCAAGAAGTTCCTGTGCTCGCTCTTCCGCCCGCTGCTCGATGA	572
Db	97	GcysHisSerAspThrGlnValPheLeuCysSerLeuPheAlaProValCys-----	114
QY	573	CCTAGACGAGACCATCCAGCATGCCACTCGCTCTGCTGTCGAGTGAAGGACCGCTGCC	632
Db	115	-LeuAspArgProIleTyrProCysArgSerLeuCysGluAlaValArgAlaGlyCysAl	134
QY	633	CCGGTTCATGCTCGGCTTCCCTCGGCGCGACATGCTTGAGTGGACGCTTCCC	692
Db	134	aProLeuMetGluAlaTyrGlyPheProTrpProGluMetLeuHisCysHisLysPhePr	154
QY	693	CCAGGACACGACCTTTGATCCCTCGCTAGCAGCGACACCTCTCCAGCCACCGA	752
Db	154	oLeuAspAsnAspLeuCysIleAlaValGlnPheGlyHis-----LeuProAlaThr--	171
QY	753	GGAAGCTCCA-----AAGTATGTGAAGCTGCAGCAATAAATAATGATGATGACAA	803
Db	172	----AlaProProValThrLysIleCysAlaGlnCysGluMetGluHisSerAlaAspGl	190
QY	804	CGACATAATGGAAGCGCTTTGATAAATGATTTTGCACCTGAAATAAAGTGAAGGAGAT	863
Db	190	y--LeuMetGluGlnMetCysSerSerAspPheValValLysMetArgIleLysGluIl	209
QY	864	AACCTACATCAACCGAGATACCAAAATCATCTGAGACCAAGACGACCACTTTACAA	923
Db	209	elysIleGluAenGlyAspArgLysLeuIleGlyAlaGlnLysLysLysLeuLeuLy	229
QY	924	GCTGAACGGTGTGTCGGAAGGAGCCTGAAGAAATCGGTGCTGTGGCTCAAGACAGCTT	983

Db	229	sSerGlyProLeuLysArgLysAspThrLysArgLeuValLeuHisMetLysAsnSerAl	249
QY	984	GCAGTGCACCTGTGAGGAGATGAACGACATCAACGCCCTATCTGGTTCATGGGACAGAA	1043
Db	249	aGlyCysProCysProGlnLeuAspSerLeuAlaGlySerPheLeuValMetGlyArgLy	269
QY	1044	ACAGGTGGGAGCTGGTGATCACCTCGTGAAGCGGTGGCAGAAAGGGGCGACAGAGATT	1103
Db	269	eValAspGlyGlnLeuLeuMetAlaValTyrArgTrpAspLysLysAsnLysGluMe	289
QY	1104	CAAG	1107
Db	289	tLys	290

Search completed: September 1, 2005, 09:37:15

Job time : 327.5 secs

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